

Result No.	Score	Query			DB	ID	Description
		Match	Length				
1	840.5	67.5	234	4	Q43404	Q43404 homo sapien	
2	90	7.2	280	6	Q9MYL6	Q9MYL6 macaca neme	
3	89.5	7.2	225	13	Q9IB42	Q9IB42 paralicthy	
4	89.5	7.2	401	2	P72902	P72902 synechocyst	
5	89.5	7.2	847	14	Q9WTS1	Q9WTS1 human immun	
6	89	7.1	169	11	Q9WY90	Q9WY90 marmota mon	
7	88	7.1	234	6	Q28320	Q28320 capra hircu	
8	87.5	7.0	896	10	Q9M9B0	Q9M9B0 arabidopsis	
9	87	7.0	2013	5	Q96216	Q96216 plasmodium	
10	86.5	6.9	217	11	Q9ER66	Q9ER66 peromyscus	
11	86.5	6.9	2195	3	Q02832	Q02832 saccharomyc	
12	86	6.9	674	3	Q06639	Q06639 saccharomyc	
13	85.5	6.9	873	10	Q9FUD8	Q9FUD8 arabidopsis	
14	85	6.8	283	10	Q9FKU2	Q9FKU2 arabidopsis	
15	85	6.8	699	14	Q9DPZ6	Q9DPZ6 human immun	
16	84.5	6.8	208	2	O68241	O68241 pantoea cit	
17	84.5	6.8	884	10	O81069	O81069 arabidopsis	
18	84	6.7	282	14	Q9IC83	Q9IC83 kaposi's sa	
19	84	6.7	544	14	O64940	O64940 avian infec	

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Db 55 ATIMVLVORTSDIPSPDNVPLKGGNCSEDLICLRAPFKKSWAYLQVAKHLNKTLS 114
QY 120 WNEGGTIGLIIYQDGNLIYQFPGLYFIVCOLFVOCNSHNSVDLTQLLINSKIKKQTLV 179
Db 115 WNKDGLHGVRYQDGNLIYQFPGLYFIVCOLFVOCNNNSVDLKXELLINKHKKQXLV 174
QY 180 TVCESGVQSKNIYQNSQFLLHYLQWNSTISVRVDFNQYVDNTFPDNLVSLVFLYSSD 239
Db 175 TVCESGMQTKHYVQNSQFLLDYLVQNTTISVNVDTXQYIDTSTFPLENVLSIFLXNSD 234

RESULT 2
QYMYL6 PRELIMINARY; PRT; 280 AA.
AC Q9MYL6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE FAS LIGAND.
GN PT-FASL OR CM-FASL OR RM-FASL.
OS Macaca nemestrina (Pig-tailed macaque),
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9545, 9541, 9544;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.nemestrina; STRAIN=PIG-TAILED MONKEY;
RA Kirii Y., Inoue T., Yoshino K.;
RT "Pig-tailed monkey Fas ligand mRNA, complete cds.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.fascicularis; STRAIN=CYNOMOLGUS MONKEY;
RA Kirii Y., Inoue T., Yoshino K.;
RT "Cynomolgus monkey Fas ligand mRNA, complete cds.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta; STRAIN=RHESUS MONKEY;
RA Kirii Y., Inoue T., Yoshino K.;
RT "Rhesus monkey Fas ligand mRNA, complete cds.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB035140; BAA90296.1;
DR EMBL; AB035138; BAA90294.1;
DR EMBL; AB035139; BAA90295.1;
DR InterPro; IPR000478;
DR Pfam; PF00229; TNF_1;
DR PRINTS; PR01234; TNECROSISFCT.
DR PROSITE; PS00251; TNF_1;
DR PROSITE; PS00049; TNF_2;
SQ SEQUENCE 280 AA; 31367 MW; F0B284D61A132EB4 CRC64;

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Query Match 7.2%; Score 90; DB 6; Length 280;
Best Local Similarity 21.1%; Pred. No. 0.84; Mismatches 75; Indels 82; Gaps 12;
Matches 52; Conservative 37;

QY 14 PSPDPAMQVQGSVAPSWRSTPWRSTRSYFYSTALVCLVAVAIILVLV----- 67
Db 59 PSLPPLPLPP-----LKKRGHSTG-----LCLLVFFVWLVALVGLGLGM 100

QY 68 -----QKSDSTPNTKAPLKGNCSEDLFCTLKS-----TPSKSW---AYLQVSK 111
Db 101 FOLFHLQ-----ELALRESTSQKHTASSLEKQIGHPSPPEKKEQKVAHLTGK 152

QY 112 HLNNTKLSWNEGGTIT---HGLIYQDGNLIYQFPGLYFIVCOLFVQ-CSN---HSDVL 163
Db 153 NSRSMPLWEYDYGIVLISGVKRYKKGLVINETGLYFVYKSVYFGSGCTNPLPSHKV-- 210

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QY 164 TLQLLINSK-----IKKOTLVTVCSG-----VQSKNIYQNSQFLLHY 202
Db 211 ---YMRNSYQPDLYMMEGKMSYCTTGQWHAHSSYLGAVFNLTSADHLYVNVSELSYN 267
QY 203 LQVNST 208
Db 268 FEESOT 273

RESULT 3
QYIB42 PRELIMINARY; PRT; 225 AA.
AC Q9IB42;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE TUMOR NECROSIS FACTOR.
OS Paralicthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectidae; Bothidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RA Hirono I., Nam B., Kurobe T., Aoki T.;
RT "Molecular cloning, characterization and expression of tumor necrosis
factor (TNF) cDNA and gene from Japanese flounder Paralicthys
olivaceus.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB040448; BAA94969.1;
DR InterPro; IPR000478;
DR Pfam; PF00229; TNF_1;
DR PRINTS; PR01234; TNECROSISFCT.
DR PROSITE; PS00049; TNF_2;
SQ SEQUENCE 225 AA; 24965 MW; 8F947FB25FC82658 CRC64;

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Query Match 7.2%; Score 89.5; DB 13; Length 225;
Best Local Similarity 25.4%; Pred. No. 0.74; Mismatches 23; Indels 11; Gaps 5;
Matches 31; Conservative 23;

QY 52 LVCLVAVAIILVLVQKKDSTPNTKAPLKGNCSE--DLFCTLKSTPSK-KSWAYL- 107
Db 10 IVALCLGVLAFAFWYTNKSEMNTSGQTAALSKQCAKTEPHNTLRQISSRAKAAIHLE 69

QY 108 ---QVSKHLNNTKLSW-NEDG---TIHGLIYQDGNLIYQFPGLYFIVCOLFVOCNSHS 160
Db 70 GRDEDEETSENKLVKNKDEGLAFTQGGFELVDNHHIIPRSLGYFVYQSAPRVSQSD 129

QY 161 VD 162
Db 130 AD 131

RESULT 4
P72902 PRELIMINARY; PRT; 401 AA.
AC P72902;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE HYPOTHETICAL 46.0 KDA PROTEIN.
GN SLR1066.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugliura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,

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RA Shimp S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.:
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
DR DNA Res. 3:109-136(1996).
DR EMBL: D90901; BAA16918.1; -
DR InterPro: IPR001296; -
DR Pfam: PF00534; Glycos_transf_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 401 AA; 45951 MW; 9A8C3E0C64933271 CRC64;

Query Match 7.2%; Score 89.5; DB 2; Length 401;
Best Local Similarity 26.6%; Pred. No. 1.4;
Matches 42; Conservative 13; Mismatches 50; Indels 53; Gaps 6;

Qy 90 DLFCFLKSTPSSKSWAYL-----QVSKHLN-----NTKLSWNEDGTIH 127
Db 47 DAFPEIKSLPKLLWLYRLPMPFSQRAKEYIQKHANFDDIIDAQGNLFPSKEE----- 101

Qy 128 GLIYQDGLIVOPGLYFIVCQLQFLVQ-----CSNHSVDLTQLLLNSKIKKQTLVTY 181
Db 102 --LKNGTLIVRSGLYAPHQFOELVQKTNLWLSGNVFKLLRLKLRKIKQKQN---- 155

Qy 182 CSEGVQSKNIYQNLQFLHYLQVNSTISVRVDNFOYV 219
Db 156 -----QN---YLLSFQKADGIILINSDELAYV 179

RESULT 5
Q9WIS1 PRELIMINARY; PRT; 847 AA.
ID Q9WIS1
AC Q9WIS1;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE ENVELOPE GLYCOPROTEIN PRECURSOR, GP160.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97NOGIL3;
RA Jonassen T.O.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=97NOGIL3;
RX MEDLINE=20092438; PubMed=10628916;
RA Jonassen T.O., Grinde B., Asjo B., Hasle G., Hungnes O.;
RT "Inter-subtype recombinant HIV-1 involving HIV-MAL-like and subtype H-
RT like sequence in four Norwegian cases.";
RL AIDS Res. Hum. Retroviruses 16:49-58(2000).
DR EMBL: AJ237565; CAB39923.2; -
DR InterPro: IPR000328; -
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
SQ SEQUENCE 847 AA; 95496 MW; E8770E4691304EB6 CRC64;

Query Match 7.2%; Score 89.5; DB 14; Length 847;
Best Local Similarity 20.9%; Pred. No. 3;
Matches 37; Conservative 37; Mismatches 56; Indels 47; Gaps 8;

Qy 71 DSTPNTTEKAPLGGNCSEDLCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLI 130
Db 138 DTNTNTSIQPSQNSCNFNTAIRDKQKVHALYFRV---DLVSDNNNTQYRLI 193

Qy 131 YQDGNLIVQ-----FPGLYFIV-----CQLQFLVQCSNHSVD- 162
Db 194 NCNTSVITQACPKVTFEPIPIHYCAPAGFAILKCNKNTFSGTGPKCNVSTVQCT-HG1KP 252
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Qy 163 -LTQLLLNSKIKKQTLVTVCESGVQSKNIYQNLQFLHY---LQVNSTISVRVDN 215
Db 253 VVSTQLLLNSLAEKVI-----IRSKNTIDNTKNIIVHFNESVOINCT----RIAN 299

RESULT 6
Q9WV90 PRELIMINARY; PRT; 169 AA.
ID Q9WV90
AC Q9WV90;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE FAS LIGAND (FRAGMENT).
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEALTHY LIVER;
RA Hodgson P.D., Grant M.D., Michalak T.I.;
RT "Perforin and Fas/Fas ligand-mediated cytotoxicity in acute and
RT chronic woodchuck viral hepatitis.";
RL Clin. Exp. Immunol. 0:0-0(1999).
DR EMBL: AF152368; AAD38387.1; -
DR InterPro: IPR000478; -
DR Pfam: PF00229; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
DR SMART: SM00207; TNF; 1.
FT NON_TER 1
FT NON_TER 169
SQ SEQUENCE 169 AA; 19274 MW; FDE395B014717B6B CRC64;

Query Match 7.1%; Score 89; DB 11; Length 169;
Best Local Similarity 24.1%; Pred. No. 0.61;
Matches 33; Conservative 24; Mismatches 42; Indels 38; Gaps 7;

Qy 97 STPSKKS---WAYLQVSKHLNNTKLSWNED---GTIHLIYQDGLIVOPGLYFIVCQ 149
Db 32 SSPDKKALRRAAHLTGKPNSSPLEWEDYGISLVYQKGLVINDTGLYFVYSK 91

Qy 150 LQFLVQ-CSN---HSVDLTQLLLNSK-----IKKQTLVTVCESG----- 185
Db 92 IYFRQSCNNQPLSHKV-----YVKNKYPQDLVLMCKGMNYCTTGQWARRSSYLGAVF 146

Qy 186 --VQSKNIYQNLQFL 200
Db 147 NFTSNDHLVNVNSEL 163

RESULT 7
Q28320 PRELIMINARY; PRT; 234 AA.
ID Q28320
AC Q28320;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TNF-ALPHA.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA Takakura H., Mori Y., Tatsumi M.;
RT "Molecular cloning of caprine TNF-alpha cDNA and its expression in
RT E.coli and insect cells.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
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DR EMBL; D86587; BAA13130.1; -
DR HSSP; P01375; 47SV.
DR InterPro; IPR000478; -
DR InterPro; IPR003636; -
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PRO1234; TNECROSISFCT.
DR PRODOM; PD00212; -; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS0049; TNF_2; 1.
DR SMART; SM00207; TNF; 1.
SQ SEQUENCE 234 AA; 25519 MW; 9768E33BBABB041 CRC64;

Query Match 7.1%; Score 88; DB 6; Length 234;
Best Local Similarity 24.1%; Pred. No. 1.1;
Matches 48; Conservative 38; Mismatches 89; Indels 24; Gaps 8;

Qy 41 SRSFYLTALVCLVAVAILVIVOKDSTPNTEKAPLKGNCSEDLFTCTLKST-- 98
Db 27 SRSWCLSLFSF--LLVAGATTFLCLHFGVIGPQREEQSP-AGPSFNRLPLVQTLRSSQ 83
Qy 99 -PSKSWAYLQVSKHLNNTKLSWNEGT-----IHGLIQDGNLIYQFGLYFVLCQLFL 153
Db 84 ASSNKPVAHV-VANISAPQLRWGSDYANALKANGVELKDNQLVPTDGLYLYSQVLEF 142
Qy 154 VQ-CSNHSVDLTQLLINSKIKKQTLVTVCES-----GVQSKNIYQNLISQFLH 201
Db 143 GHGCPSTPLFT-HTISRIAYSTQKVNLSAISKPHCHRETPEGAERKWPYEPYQGGVF 201
Qy 202 YLQNSTISVRVDFQYVD 220
Db 202 QLEKGRDLSAEINOPEYLD 220

RESULT 8
Q9M9B0 PRELIMINARY; PRT; 896 AA.
AC Q9M9B0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE F27J15.13.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Kim C., Altafi H., Bei Q., Chin C., Chlou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F27J15 from chromosome
RT I."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AC016041; AAF69701.1; -
DR InterPro; IPR00719; -
DR InterPro; IPR001245; -
DR InterPro; IPR001611; -
DR InterPro; IPR002290; -
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00560; LRR; 3.
DR PRINTS; PR00019; LEURICHKPT.
DR PRINTS; PR00109; TYRKINASE.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR SMART; SM00220; S_TKC; 1.

KW ATP-binding; Serine/threonine-protein kinase; Transferase;
KW Tyrosine-protein kinase.
SQ SEQUENCE 896 AA; 99724 MW; A24500615125A15C CRC64;

Query Match 7.0%; Score 87.5; DB 10; Length 896;
Best Local Similarity 21.4%; Pred. No. 5;
Matches 43; Conservative 42; Mismatches 59; Indels 57; Gaps 11;

Qy 9 GSCGAPSPDPAMQVQPGSVASPRWSTPRWSTSRSYFLSTTALVCLVAVAILVLVVQ 68
Db 502 GPCGN-----KPGEGGPKKSI-----IVPVSSVALITALIA-AULVFLVLR 543
Qy 69 KDDSTPNTEKAPLKGNCSEDLFTCTLKSTP-----SKSWAYLQVSKHLNNTKLSWNEG 124
Db 544 KKN--PSRSK-----ENGRTSR-----SSEPPRTTKKKKTYVEVTEWNTNFRSVLGGG 591
Qy 125 THGLIYQDGNLIYQFGLYFVLCQLFVOCNSNHS-----VDLTQLLINSIKK 175
Db 592 --FGMYVHG-----YVNGREQVAVKVLASHKGKQFKAEEVLLLRVHHK-NL 637
Qy 176 QTLVTVCSGVSQSKNIYQNLIS 196
Db 638 VSLVGyceKGEKALALYVEYMA 658

RESULT 9
Q96216 PRELIMINARY; PRT; 2013 AA.
AC Q96216;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE PREDICTED MEMBRANE ASSOCIATED PROTEIN.
GN FFB0615C.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99021743; PubMed=9804551;
RA Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind L.,
RA Koenin E.V., Shallom S., Mason T., Yu K., Fujii C., Pederson J.,
RA Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Perlea M.,
RA Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
RA Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
RT falciparum."
RL Science 282:1126-1132(1998).
DR EMBL; AB001406; AAC71912.1; -
SQ SEQUENCE 2013 AA; 243596 MW; 7AD1F050E79C8731 CRC64;

Query Match 7.0%; Score 87; DB 5; Length 2013;
Best Local Similarity 23.9%; Pred. No. 13;
Matches 34; Conservative 31; Mismatches 49; Indels 28; Gaps 7;

Qy 88 SEDLFTCTLKSTPSSKSWAYLQVSKHLNNTKLSWNEGTTHGLIYQDGNLIYQFGLYFIV 147
Db 16 SDNIFCLKD-----GYICFMNLLN-----NEKKYLYTCSQDEGYAQY---YFDV 59
Qy 148 COLQFLVQCSNHSVDLTQLLI-----NSKIKKQTLVTVCSGVSQSKNIYQNLISQFL 200
Db 60 VKCRYEKKEEDCKNKTINIMLQENKLIKETCYI---KNVVTNKIYHTL--FLVINK 114
Qy 201 HYLQVNSTISVRVDFQYVDN 222
Db 115 HYHNILCSLSFENNSFEILNTN 136

RESULT 10
Q9ERG6 PRELIMINARY; PRT; 217 AA.
ID Q9ERG6
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AC Q9RC6;
AD 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE TUMOR NECROSIS FACTOR ALPHA (FRAGMENT).
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OC NCBI_TaxID=10042;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Herbat M.M., Schountz T.;
RT "Cloning of the deer mouse interferon gamma, interleukin-10 and tumor
RT necrosis factor genes.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF307013; AAC30264.1;
FT NON_TER 1
FT NON_TER 217
FT SEQUENCE 217 AA; 23964 MW; D6F90C74C0B3021F CRC64;
SQ

Query Match 6.9%; Score 86.5; DB 11; Length 217;
Best Local Similarity 23.6%; Pred. No. 1.4;
Matches 53; Conservative % 38; Mismatches 95; Indels 39; Gaps 11;

QY 19 AMOVQPGSVASPRWSTRPWSTRSYFVLS--TTALVCLVAVAILVLVWOKKDSPTNTT 77
DB 5 AEALPKKANGPONSSRCCLSLFLLVAGATYFCLL----NFGVIGPOREKFFPN-- 58
QY 78 EKAPLKGNGCEDLFTIKST--PSKKSWAYLQVSKHLNNTKLSWNEDGT----IHGLI 130
DB 59 -NLPIIGSMAQT---LTLRSSQNSDKPVAHV-VANHQVDEQLWLSRRANALLANGMD 113
QY 131 YQGNLLIVQPGIFYVCQQLFVQ-CSN-----HSVD-----LTLOLLINSKIKK 175
DB 114 LKDNQLVIPADGLVLYVSQVLFKGQGSNYVLLFHTVSRFAVSIEDKYNLLSAIKSPCK 173
QY 176 QTLIVTCESGVQSKNIYQNLQSQFLHLHYLVNSTISVRVDFQYVD 220
DB 174 ET-----PEGSELAPWTEPIYLGGVFQLEKGRUSAEVNLPKYLD 213

RESULT 11
Q02822 PRELIMINARY; PRT; 2195 AA.
AC Q02822;
AD 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE VESICLE COAT PROTEIN SEC16P.
OS SEC16.
OC Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OC NCBI_TaxID=4932;
RN [1]
RN SEQUENCE FROM N.A.
RC MEDLINE=87089718; PubMed=3025612;
RA Baker H.V.;
RT "Glycolytic gene expression in Saccharomyces cerevisiae: nucleotide
RT sequence of GCRI, null mutants, and evidence for expression.";
RL Mol. Cell. Biol. 6:3774-3784 (1986).
RN [2]
RN SEQUENCE FROM N.A.
RC MEDLINE=88111651; PubMed=2892678;
RA Velours J., Durrens P., Aigle M., Guerin B.;
RT "ATP4, the structural gene for yeast F0F1 ATPase subunit 4.";
RL Eur. J. Biochem. 170:637-642 (1988).
RN [3]
RN SEQUENCE FROM N.A.
RC MEDLINE=92195335; PubMed=1312673;

```

RA Davis J.L., Kunisawa R., Thorner J.;  
 RT "A presumptive helicase (MOR1 gene product) affects gene expression  
 RT and is required for viability in the yeast *Saccharomyces cerevisiae*.";  
 RL Mol. Cell. Biol. 12:1879-1892(1992).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-95274317; PubMed-7754704;  
 RA Schnall R., Mannhaupt G., Stucka R., Tauer R., Ehnlé S.,  
 RT Schwarzlose C., Vetter I., Feldmann H.;  
 RT "Identification of a set of yeast genes coding for a novel family of  
 RT putative Arpases with high similarity to constituents of the 26S  
 RT protease complex.";  
 RL Yeast 10:1141-1153(1994).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-95286583; PubMed-7768896;  
 RA Leidich S.D., Kostova Z., Latek R.R., Costello L.C., Drapp D.A.,  
 RA Gray W., Fassler J.S., Orlean P.;  
 RT "Temperature-sensitive yeast GPI anchoring mutants gpi2 and gpi3 are  
 RT defective in the synthesis of N-acetylglucosaminyl  
 RT phosphatidylinositol. Cloning of the GPI2 gene.";  
 RL J. Biol. Chem. 270:13029-13035(1995).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-96017704; PubMed-7593161;  
 RA Espenshade P., Gimeno R.E., Holzmacher E., Teung P., Kaiser C.A.;  
 RT "Yeast SEC16 gene encodes a multidomain vesicle coat protein that  
 RT interacts with Sec23p.";  
 RL J. Cell Biol. 131:311-324(1995).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-97313271; PubMed-9169875;  
 RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansoorge W.,  
 RA Araujo R., Aparicio A., Barrell B., Badcock K., Benes V., Botstein D.,  
 RA Bowman S., Bruckner M., Carpenter J., Cherry J.M., Chung E.,  
 RA Churcher C., Coster F., Davis K., Davis R.W., Dietrich F.S.,  
 RA Delius H., DiPaolo T., Dubois E., Dusterhoff A., Duncan M., Floeth M.,  
 RA Fortin N., Friesen J.D., Fritz C., Goffeau A., Hall J., Hebling U.,  
 RA Heumann K., Hilbert H., Hillier L., Hunnicke-Smith S., Hyman R.,  
 RA Johnston M., Kalman S., Kleine K., Komp C., Kurdi O., Lashkari D.,  
 RA Lew H., Lin A., Lin D., Louis E.J., Marathe R., Messenguy F.,  
 RA Mewes H.W., Mirtipati S., Moestl D., Muller-Auer S., Namath A.,  
 RA Nentwich U., Osafner P., Pearson D., Petel F.X., Pohl T.M.,  
 RA Purnelle D., Schaefer M., Scharfe M., Scherens B., Schramm S.,  
 RA Schroeder M., Sdicu A.M., Tettelin H., Urrestazu L.A., Ushinsky S.,  
 RA Vierendeels F., Vissers S., Voss H., Walsh S.V., Wambutt R., Wang Y.,  
 RA Wedler E., Wedler H., Winnett E., Zhong W.W., Zollner A., Vo D.H.,  
 RA Hani J.;  
 RT "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome XVI.";  
 RL Nature 387:0-0(0).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RA Hall J., Ahmed A., Bussey H., Fortin N., Friesen J.D., Storms R.K.,  
 RA Vo D.H., Wang Y., Winnett E.;  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [9]  
 RP SEQUENCE FROM N.A.  
 RA Bussey H.;  
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.  
 RN [10]  
 RP SEQUENCE FROM N.A.  
 RA Jia Y., Cherry J.M.;  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U41849; AAB68254.3; -.  
 DR SGD: S00060006; SEC16.  
 SQ SEQUENCE 2195 AA; 241694 MW; 757B7A7231BEE6F0 CRC64;  
 SQ

Query Match 6.9%; Score 86.5; DB 3; Length 2195;  
 Best Local Similarity 20.9%; Pred. No. 16;  
 Matches 53; Conservative 39; Mismatches 87; Indels 75; Gaps

QY 26 SVASPRWRSTRP-----WRSTSRSYF-----YLSITALVCLVVA 58

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Query Match      6.98; Score 86.5; DB 3; Length 2195;
Best Local Similarity 20.98; Pred. No. 16;
Matches 53; Conservative 39; Mismatches 87; Indels 75; Gaps 13;

QY 26 SVASPWRSRDP-----WRSTRSYF-----YLSSTALVCLVVA 58

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|||||
Db 970 SVAPPROENPIKIDNEALLRRPPIFHSAANKVYVAVPPIDQSOYMISSSIVOSIKV 1029
QY 59 VAILVLVVOKKD---STNTTEKAPLKGNCSEDLFTCLKSTPSKKS-----WAYLOV 109
Db 1030 TPI--DOIIPNDMLKSPFGPLGSAKKKDLTKWMTTIKSIENESSTDMTIWQLLEM 1087
QY 110 SKHLNNTKLSWNEGTIHLIYODGNLIV-----QFGLY--FIVCQLQFL--VQ 155
Db 1088 KL---NDKVNWK---NISKLYNSDELLMYLSQFPFGMDIPNAYRLDINCOMRVLAFLQ 1141
QY 156 CSNHSV-----DLTQLLINSKIKKOTLVTV-----ESGVSKNYIQNLSOFLH 201
Db 1142 TGNHDEALRLALSKRDAYATALLVGLSLMGDRWSEVIQKLYEGTAGPNDQKELAFLLL 1201
QY 202 YLOV---NSTISVR 212
Db 1202 IFOVFVGNKMAIK 1215

RESULT 12
Q06629 PRELIMINARY; PRT; 674 AA.
AC Q06629;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE SIMILARITY TO STREPTOCOCCUS PROTEIN V.
GN D9740.10 OR PLO2.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favell A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
RA Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
RA Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,
RA Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
RA Taich A., Travaskis E., Vignati D., Wilcox L., Wohlman P., Vaudin M.,
RA Wilson R., Waterston R.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ding H.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Jia Y., Cherry J.M.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U28374; AAB64731.1; -.
DR SGD; S0002703; PLO2.
DR InterPro; IPR000255; -.
DR InterPro; IPR001871; -.
DR PROSITE; PS00036; BZIP_BASIC; UNKNOWN_1.
DR PROSITE; PS00012; PHOSPHOPANTHETINE; UNKNOWN_1.
SQ SEQUENCE 674 AA; 77059 MW; CE768CBCC84CCD97 CRC64;

Query Match 6.9%; Score 86; DB 3; Length 674;
Best Local Similarity 25.0%; Pred. NO. 5.1;
Matches 40; Conservative 30; Mismatches 60; Indels 30; Gaps 9;

QY 70 KDSTPNTTEKAPLKGNCSE-----EDFCTLKSTPSKK-----SWAYLOVSKHLNNTK- 117
||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 192 KGGTPNSVSSSTSSNSNSTSYTGSKDDYDYSVKRLNKRKINTDMLFLATTKKHKHDQY 251
||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 118 LSWNEGTIHLIYODGNLIVQFPGLYFI-----VCQLQLVQCSNHSVDLTQLLIN 170
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|||||
Db 252 LLANYD--IDMIISDFPMLELPAQVLRNANKRPIIKLLVQ---NSPD---HYLLD 303
QY 171 SKIKKQTLVT--VCESG-VQSKNYIQNLSOFLHLYQVNS 207
Db 304 SEIKSSVKSHLSNNGHVDSDSQEYEIKSSLLYFLQARN 343

RESULT 13
Q9FID8 PRELIMINARY; PRT; 873 AA.
AC Q9FID8;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE RECEPTOR-LIKE PROTEIN KINASE.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=99156233; PubMed=10048488;
RA Asamizu E., Sato S., Kaneko T., Nakamura Y., Kotani H., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VIII.
RT Sequence features of the regions of 1,081,958 bp covered by seventeen
RT physically assigned P1 and TAC clones."
RL DNA Res. 5:379-391(1998).
DR EMBL; AB016892; BAB10824.1; -.
KW Kinase.
SQ SEQUENCE 873 AA; 97164 MW; B2879DE5BC7337A7 CRC64;

Query Match 6.9%; Score 85.5; DB 10; Length 873;
Best Local Similarity 23.5%; Pred. No. 7.5;
Matches 47; Conservative 43; Mismatches 79; Indels 31; Gaps 11;

QY 9 GSCGAPSDPAMQVQGSVAPWRSTSRYSYFLSTALVCLVAVAI---ILV 64
| : ||| | : : : : : : : : : : : : : : : : : : : : : : : :
Db 410 GNLAGPNPDL--VSPDLI--PNRAT-PRIRKKNKSHLPLTAVGSLVLA MFVGV 464
| : ||| | : : : : : : : : : : : : : : : : : : : : : : : :
QY 65 LVQKKDSTPTTEK-APLKGNCSEDLFTCLKSTPSK--KSWAYLOVSKHLNNTKLSWN 121
| : ||| | : : : : : : : : : : : : : : : : : : : : : : : :
Db 465 IMKKKKSKSTNSWCPLPHGTDSTNT-KPAKSLPADLCRRFSIFEIKSATNDF----- 518
| : ||| | : : : : : : : : : : : : : : : : : : : : : : : :
QY 122 EDGTIHGL-----IYQDGNLIVQFGLYFIVCQLQLVQCSNHSVDLTQLLINSKIKQ 176
| : ||| | : : : : : : : : : : : : : : : : : : : : : : : :
Db 519 EDKLIIGVGFGSVYKG-----QIDGGATLVAVKRLKLEITSNQAKFEFETEMLSKLRHV 573
| : ||| | : : : : : : : : : : : : : : : : : : : : : : : :
QY 177 TLVTV---CESGVQSKNIYQ 193
| : ||| | : : : : : : : : : : : : : : : : : : : : : : : :
Db 574 HLVSLLIGCYCEDNEMLVAYE 593
| : ||| | : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
Q9FKU2 PRELIMINARY; PRT; 283 AA.
AC Q9FKU2;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE GENOMIC DNA, CHROMOSOME 5, P1 CLONE:MDA7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
```



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2001, 10:23:15 ; Search time 19.38 Seconds  
(without alignments)  
422.449 Million cell updates/sec

Title: US-09-628-126-6  
Perfect score: 1246  
Sequence: 1 MPEGLQAGSCGAPSPDPAM.....DTNTPPLDNLVSLYSSSD 239

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1246	100.0	239	1 TNF8_MOUSE	P32972 mus musculus
2	860.5	69.1	234	1 TNF8_HUMAN	P32971 homo sapien
3	123	9.9	279	1 FASL_MOUSE	P41047 mus musculus
4	102	8.2	278	1 FASL_RAT	P36940 rattus norv
5	91	7.3	309	1 41BL_MOUSE	P41274 mus musculus
6	89.5	7.2	235	1 TNFA_PERLE	P36939 peromyscus
7	87	7.0	281	1 FASL_HUMAN	P48023 homo sapien
8	86.5	6.9	233	1 TNFA_MACMU	P48094 macaca mula
9	86.5	6.9	2194	1 SC16_YEAST	P48415 saccharomyc
10	85	6.8	291	1 TN10_MOUSE	P50592 mus musculus
11	84.5	6.8	525	1 C307_DROME	Q9vrm7 drosophila
12	83.5	6.7	201	1 TNFB_MACMU	Q9xt48 macropus eu
13	83.5	6.7	233	1 TNFA_MACFA	P79337 macaca fasc
14	82.5	6.6	233	1 TNFA_PAPHU	O77510 papio hamad
15	82.5	6.6	965	1 APN_MOUSE	P97449 mus musculus
16	82.5	6.6	1078	1 S24A_HUMAN	O95486 homo sapien
17	82	6.6	234	1 TNFA_SHEEP	P23383 ovis aries
18	81.5	6.5	233	1 TNFA_CANFA	P51742 canis famil
19	81	6.5	460	1 ENV_HV123	P12491 human immun
20	80.5	6.5	1376	1 RPOD_ARATH	P56764 arabidopsis
21	79.5	6.4	383	1 COS7_YEAST	Q07788 saccharomyc
22	79	6.3	229	1 TNFA_CEREL	P51743 cercus elap
23	79	6.3	851	1 NUD1_YEAST	P32336 saccharomyc
24	78.5	6.3	234	1 TNFA_HORSE	P29553 equus cabal
25	78.5	6.3	235	1 TNFA_RAT	P16599 rattus norv
26	78.5	6.3	507	1 C392_DROME	P82713 drosophila
27	78.5	6.3	816	1 NEL2_RAT	O62918 rattus norv
28	78.5	6.3	1150	1 IRR1_YEAST	P40541 saccharomyc
29	78	6.3	396	1 BMP2_HUMAN	P13643 homo sapien
30	78	6.3	856	1 ENV_HV1MN	P05877 human immun
31	77.5	6.2	178	1 IL10_MACFA	P79338 macaca fasc
32	77.5	6.2	463	1 YKN3_YEAST	P36066 saccharomyc
33	77.5	6.2	1583	1 M1S4_SCHPO	Q09725 schizosacch

## ALIGNMENTS

```

RESULT 1
TNF8_MOUSE
ID TNF8_MOUSE STANDARD; PRT; 239 AA.
AC P32972;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD30 LIGAND (CD30-L).
GN TNFSF8 OR CD30LG OR CD30L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=93313964; Pubmed=8391931;
RA Smith C.A., Gruess H.-J., Davis T., Anderson D., Farrah T.,
RA Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA Grabstein K.H., Gliniak B., McAllister I.B., Fanslow W., Alderson M.,
RA Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.;
RT "CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
RT ligand defines an emerging family of cytokines with homology to
TNF.";
RL Cell 73:1349-1360(1993).
CC -!- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
CC T CELLS.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC PIR; B40710; B40710.
CC MGD; MGI:88328; Tnfsf8.
CC InterPro: IPR000478; -.
CC Pfam; PF00229; TNF; 1.
CC PROSITE; PS00251; TNF_1; 1.
CC PROSITE; PS50049; TNF_2; 1.
CC Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
CC DOMAIN 1 43 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 44 67 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
CC DOMAIN 68 239 EXTRACELLULAR (POTENTIAL).
CC CARBOHYD 75 75 N-LINKED (GLCNAC...) (POTENTIAL).
CC CARBOHYD 86 86 N-LINKED (GLCNAC...) (POTENTIAL).
CC CARBOHYD 114 114 N-LINKED (GLCNAC...) (POTENTIAL).
CC CARBOHYD 158 158 N-LINKED (GLCNAC...) (POTENTIAL).
CC CARBOHYD 194 194 N-LINKED (GLCNAC...) (POTENTIAL).
CC CARBOHYD 206 206 N-LINKED (GLCNAC...) (POTENTIAL).
CC SEQUENCE 239 AA; 26519 MW; 29003157DD425159 CRC64;

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34 77 795 1 SYFB_BUCAI P57230 buchnera ap
35 76.5 6.1 317 1 TN11_HUMAN O14788 h tumor nec
36 76.5 6.1 345 1 OPCM_BOVIN P11834 bos taurus
37 76.5 6.1 1073 1 HSER_PIG P55204 sus scrofa
38 76 6.1 234 1 TNFA_CAYPO Q9v557 drosophila
39 76 6.1 520 1 C4P2_DROME P51435 cavia porce
40 75.5 6.1 178 1 IL10_CERTO Q9v557 cercopithecus
41 75.5 6.1 383 1 COS5_YEAST P47187 saccharomyc
42 75.5 6.1 1178 1 PH81_YEAST P17442 saccharomyc
43 75 6.0 179 1 I10H_HSYE2 Q89451 equine herp
44 75 6.0 524 1 2A5G_HUMAN Q13362 h serine/th
45 75 6.0 524 1 2A5G_RABIT Q28651 o serine/th

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Query Match      100.0%; Score 1246; DB 1; Length 239;
Best Local Similarity 100.0%; Pred. No. 9.3e-107;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPGLQAGSGCAPSPDPAMQVQPGSVASPMWRSTPRWSTRSFYSLSTALVCLVAV 60
D 1 MEPGLQAGSGCAPSPDPAMQVQPGSVASPMWRSTPRWSTRSFYSLSTALVCLVAV 60
QY 61 IILVLVQKDSPTNTTEKAPLKGNCSEDLCTLKSTPSKSWAYLOVSKHLNNTKLS 120
D 61 IILVLVQKDSPTNTTEKAPLKGNCSEDLCTLKSTPSKSWAYLOVSKHLNNTKLS 120
QY 121 NEDGTIHLIYQDGNLIYQVFPGLYFIVQQLQFLVQCSNHSVDLTQLLNSIKKQTLV 180
D 121 NEDGTIHLIYQDGNLIYQVFPGLYFIVQQLQFLVQCSNHSVDLTQLLNSIKKQTLV 180
QY 181 VCESGVQSKNIYQNSQFLHLYQVNSTISVRDNFQYVDNTFPDLNVLVSFLYSSD 239
D 181 VCESGVQSKNIYQNSQFLHLYQVNSTISVRDNFQYVDNTFPDLNVLVSFLYSSD 239

RESULT 2
TNF8_HUMAN
ID TNF8_HUMAN STANDARD; PRT; 234 AA.
AC P32971;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CD30 LIGAND (CD30-L) (CD153 ANTIGEN).
GN TNFSF8 OR CD30LG OR CD30L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=93313964; PubMed=8391931;
RA Smith C.A., Gruess H.-J., Davis T., Anderson D., Farrah T.,
RA Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA Grabstein K.H., Gliniak B., McAllister I.B., Fanslow W., Alderson M.,
RA Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.;
RT "CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
RT ligand defines an emerging family of cytokines with homology to
RT TNF."
RL Cell 73:1349-1360(1993).
CC -!- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
CC T CELLS.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD153 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd153.htm".
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CC EMBL; L09753; AAA74594.1; -
CC PIR; A0710; A40710.
CC MIM; 603875; -
CC InterPro; IPR000478; -
CC Pfam; PF00229; TNF; 1.
CC PROSITE; PS00251; TNF.1; 1.
CC PROSITE; PS50049; TNF.2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 62 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 63 234 EXTRACELLULAR (POTENTIAL).

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FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 234 AA; 26017 MW; C653615682305B1B CRC64;

Query Match      69.1%; Score 860.5; DB 1; Length 234;
Best Local Similarity 69.6%; Pred. No. 1.5e-71;
Matches 167; Conservative 28; Mismatches 38; Indels 7; Gaps 2;

QY 1 MEPGLQAGSGCAPSPDPAMQVQPGSVASPMWRSTPRWSTRSFYSLSTALVCLVAV 59
D 1 MDPGLQALNGMAPPDGTAMHVPAAGSVAS-----HLGTTSRSYFYLTATLCLVFTV 54
QY 60 AITLVLVQKDSPTNTTEKAPLKGNCSEDLCTLKSTPSKSWAYLOVSKHLNNTKLS 119
D 60 AITLVLVQKDSPTNTTEKAPLKGNCSEDLCTLKSTPSKSWAYLOVSKHLNNTKLS 119
QY 120 WNEDGTIHLIYQDGNLIYQVFPGLYFIVQQLQFLVQCSNHSVDLTQLLNSIKKQTLV 179
D 120 WNEDGTIHLIYQDGNLIYQVFPGLYFIVQQLQFLVQCSNHSVDLTQLLNSIKKQTLV 179
QY 115 WNKDGILHGVYQDGNLIYQVFPGLYFIVQQLQFLVQCPNNSVDLKLKLELLINKHKQALV 174
D 115 WNKDGILHGVYQDGNLIYQVFPGLYFIVQQLQFLVQCPNNSVDLKLKLELLINKHKQALV 174
QY 180 TVCESGVQSKNIYQNSQFLHLYQVNSTISVRDNFQYVDNTFPDLNVLVSFLYSSD 239
D 175 TVCESGMQTRHVVQNSQFLHLYQVNSTISVRDNFQYVDNTFPDLNVLVSFLYSSD 234

RESULT 3
FASL_MOUSE
ID FASL_MOUSE STANDARD; PRT; 279 AA.
AC P41047; Q61217; Q9RLF2;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FAS ANTIGEN LIGAND.
GN TNFSF6 OR APTILG1 OR FASL OR GLD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RX MEDLINE=94185175; PubMed=7511063;
RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
RA Suda T., Nagata S.;
RT "Generalized lymphoproliferative disease in mice, caused by a point
RT mutation in the Fas ligand."
RL Cell 76:969-976(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
RC STRAIN=C57BL/6;
RX MEDLINE=95388076; PubMed=7544870;
RA Peitsch M.J., Tschopp J.J.;
RT "Comparative molecular modelling of the Fas-ligand and other members
RT of the TNF family."
RL Mol. Immunol. 32:761-772(1995).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=95196085; PubMed=7889405;
RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a
RT TNF family gene cluster."
RL Immunity 1:131-136(1994).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RC STRAIN=BA1B/C;
RA Fenner M.H., Shioda T., Isselbacher K.J.;
RT "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in
RT two amino acids."
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

```

[5] SEQUENCE FROM N.A. (ISOFORM FASLS).

RC STRAIN=C3H; TISSUE=Spleen;

RX MEDLINE=20021694; PubMed=10552956;

RA Ayroldi E., D'Adamo F., Zollo O., Agostini M., Moraca R.,

RA Cannarile L., Migliorati G., Delfino D.V., Riccardi C.;

RT "Cloning and expression of a short Fas ligand: A new alternatively

RT spliced product of the mouse Fas ligand gene.";

RL Blood 94:3456-3467(1999).

[6]

RN CHARACTERIZATION OF VARIANT GLD.

RX MEDLINE=96091792; PubMed=7495745;

RA Hahne M., Peitsch M.C., Irmeler M., Schroeter M., Lowin B.,

RA Rousseau M., Bron C., Renno F., French L., Tschopp J.;

RT "Characterization of the non-functional Fas ligand of gld mice.";

RL Int. Immunol. 7:1381-1386(1995).

CC -!- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT

CC TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN

CC CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.

CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF

CC PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE

CC T CELLS, OR BOTH.

CC -!- SUBUNIT: HOMOTRIMER (PROBABLE).

CC -!- SUBCELLULAR LOCATION: ISOFORM FASL IS A TYPE II MEMBRANE PROTEIN.

CC ISOFORM FASLS IS SOLUBLE.

CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; FASL (SHOWN HERE) AND FASLS; ARE

CC PRODUCED BY ALTERNATIVE SPLICING. ISOFORM FASL MEDIATES APOPTOSIS

CC WHILE ISOFORM FASLS PREVENTS APOPTOSIS INDUCED BY FAS/FASL

CC INTERACTION.

CC -!- DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERALIZED

CC LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DISEASE

CC RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION.

CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

CC

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CC

DR EMBL; U06948; AAA17800.1; -

DR EMBL; U10984; AAA19778.1; -

DR EMBL; S76752; AAB33780.1; -

DR EMBL; U58995; AAB02915.1; -

DR EMBL; AF119335; AAD52106.1; -

DR HSSP; P01375; 2TUN.

DR MGD; MGI:99255; Fasl.

DR InterPro; IPR000478; -

DR Pfam; PF00229; TNF; 1.

DR PROSITE; PS00251; TNF\_1; 1.

DR PROSITE; PS50049; TNF\_2; 1.

KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis;

KW Disease mutation; Alternative splicing.

FT DOMAIN 1 78 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 79 100 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

FT DOMAIN 101 279 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 4 69 PRO-RICH.

FT DOMAIN 45 51 POLY-PRO.

FT DISULFID 200 231 BY SIMILARITY.

FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARSPIC 1 210 MISSING (IN ISOFORM FASLS).

FT VARIANT 184 184 T -> A (IN STRAIN BALB/C).

FT VARIANT 218 218 E -> G (IN STRAIN BALB/C).

FT VARIANT 273 273 F -> L (IN GLD; ABOLISHES BINDING OF FASL

FT TO ITS RECEPTOR).

SEQUENCE 279 AA; 31442 MW; 37972E2728E0A1CA CRC64;

Query Match 9.9%; Score 123; DB 1; Length 279;

Best Local Similarity 22.5%; Pred. No. 0.00043;

Matches 55; Conservative 43; Mismatches 96; Indels 50; Gaps 11;

QY 10 SCG-----APSPDPAMQVPGSVASPRWSTPRWSTSR-----YFVLSITALV 53

DB 34 SCGPRGPQRRPPPPPPVSPPLPPPLPLPLPLPLKDKKDHNTNWLPLPVFFWLVVALV 93

QY 54 CLVAVAILVLVQKDSPTNTEKAPLGGKNCSEDLFTLKSTPSKK-----SWAYLQV 109

DB 94 GM--GLGMVQLPHLQKELAELEFNTQSLKVSFEKQI--ANPSTPEKKEPRSVAHLTG 149

QY 110 SKHLNNTKLSWNE--GT--IHGLIYQDGNLIVQFGLFIVCOLQFLVQ--CSNHSVDLTL 165

DB 150 NPHSISIPLEWEDTYGTALISGKVGKGLVNETGLTFYVSKYVFRGSCNNQPLNHKV 209

QY 166 QLLINSK-----IKQTLVTVCESG-----VQSKNIYONLSQFLLHLVQ 204

DB 210 YMR-NSKYPEDVLVMEERKLNVCYTGQIWAHSSYLGAVENTLTSADHLVYNISQLSINF 268

QY 205 VNST 208

DB 269 ESKT 272

RESULT 4

FASL\_RAT

ID FASL\_RAT STANDARD; PRT; 278 AA.

AC P36940;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE FAS ANTIGEN LIGAND.

GN TNFSF6 OR APTILG1 OR FASL.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

[1]

RN SEQUENCE FROM N.A.

RX MEDLINE=94084792; PubMed=7505205;

RA Suda T., Takahashi T., Golstein P., Nagata S.;

RT "Molecular cloning and expression of the Fas ligand, a novel member

RT of the tumor necrosis factor family.";

RL Cell 75:1169-1178(1993).

CC -!- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT

CC TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN

CC CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.

CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF

CC PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE

CC T CELLS, OR BOTH.

CC -!- SUBUNIT: HOMOTRIMER (PROBABLE).

CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED

CC INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL

CC SURFACE.

CC -!- TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND

CC THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES,

CC KIDNEY AND LUNG.

CC -!- INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.

CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

CC

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CC

DR EMBL; U03470; AAC52129.1; -

DR InterPro; IPR000478; -

DR Pfam; PF00229; TNF; 1.

DR PROSITE; PS00251; TNF\_1; 1.



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CC  EXTRACELLULAR SOLUBLE FORM.
CC  -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC  PROTEOLYTIC PROCESSING.
CC  -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC  CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC  AND MALNUTRITION.
CC  -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; M59233; AAA40596.1; -
CC  HSP; P01375; 2TUN.
CC  InterPro; IPR000478; -
CC  InterPro; IPR002959; -
CC  Pfam; PF00229; TNF; 1.
CC  PRINTS; PR01234; TNCRSISFCT.
CC  PRINTS; PR01235; TNFALPHA.
CC  PROSITE; PS00251; TNF_1; 1.
CC  PROSITE; PS50049; TNF_2; 1.
CC  Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
CC  PROPEP 1 79
CC  CHAIN 80 235
CC  TRANSMEM 36 56
CC  DISULFID 148 179
CC  CARBOHYD 86 86
CC  SEQUENCE 235 AA; 25822 MW; 235A5CFC9F9AC624 CRC64;
CC  FT
CC  KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
CC  FT PROPEP 1 79
CC  FT CHAIN 80 235
CC  FT TRANSMEM 36 56
CC  FT DISULFID 148 179
CC  FT CARBOHYD 86 86
CC  FT SEQUENCE 235 AA; 25822 MW; 235A5CFC9F9AC624 CRC64;
CC  SQ
CC  Query Match 7.2%; Score 89.5; DB 1; Length 235;
CC  Best Local Similarity 23.6%; Pred. No. 0.4;
CC  Matches 53; Conservative 39; Mismatches 94; Indels 39; Gaps 11;
CC  QY 19 AMQVQGSVASPRWRTPMRSTRSYFLS-TTALVCLVAVAILLVLVQKDKSTPTNT 77
CC  DB 13 ABEALPKAWGPQSSRCILSLFSLVAGATFLCLL-----NFGVIGPQREKFPN-- 66
CC  QY 78 EKAPLGGNCSEDLFTLKTST---PSKKWYAYLOVSKHLNKLWNEDGT-----IHGLI 130
CC  DB 67 -NLPIIGSMAQT---LTLRSSQNSDKPAHV-VANHOVDQELWLSRGANALLANGMD 121
CC  QY 131 YDGNLIVQPGLYFYICQLQFLVQ-CSN-----HSVD-----LTLQLLNSIKK 175
CC  DB 122 LKDNQLVIPADGLYLYVSQVLFKQGGSSVLLTHTVSRFAVSVDKVNLLSAIKSPCKP 181
CC  QY 176 QTLVTVCSGVSQSKNIYQNLISQFLHLYLVQNSTISVRVDNFQYVD 220
CC  DB 182 ET-----PEGSELKPWEPIYLGVSFQLEKGDRLSAEVLNPKYLD 221
CC  RESULT 7
CC  ID FASL_HUMAN STANDARD; PRT; 281 AA.
CC  AC P48023;
CC  DT 01-FEB-1996 (Rel. 33, Created)
CC  DT 01-FEB-1996 (Rel. 33, Last sequence update)
CC  DT 01-OCT-2000 (Rel. 40, Last annotation update)
CC  DE FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL).
CC  GN TNFSF6 OR APTL1 OR FASL.
CC  OS Homo sapiens (human).
CC  OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC  OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC  OX NCBI_TaxID=9606;
CC  RN [1]
CC  RP SEQUENCE FROM N.A.
CC  RX MEDLINE=95105731; PubMed=7528780;
CC  RA Alderson M.;
CC  RT "Fas ligand mediates activation-induced cell death in human T
```

```
RT lymphocytes."
RN J. Exp. Med. 181:71-77(1995).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=95127560; PubMed=7826947;
RA Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
RA "Human Fas ligand: gene structure, chromosomal location and species
RT specificity."
RL Int. Immunol. 6:1567-1574(1994).
RN [3]
RN SEQUENCE FROM N.A.
RA Schaeublein C.E., Poehmann R., Philippsen P., Eibel H.;
RN Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RX MEDLINE=95071350; PubMed=7980502;
RA Mita E., Hayashi N., Iio S., Takehara T., Hijioke T., Kasahara A.;
RA Fusamoto H., Kamada T.;
RT "Role of Fas ligand in apoptosis induced by hepatitis C virus
RN infection."
RL Biochem. Biophys. Res. Commun. 204:468-474(1994).
RN [5]
RN SEQUENCE FROM N.A.
RA Wilkinson J.;
RN Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RN SEQUENCE OF 1-10 FROM N.A.
CC TISSUB-Blood;
CC Matsumura M., Nakanishi Y., Ohba Y.;
CC Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
CC TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
CC CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
CC PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
CC T CELLS, OR BOTH.
CC -!- SUBUNIT: HOMOTRIMER (PROBABLE).
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
CC INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
CC SURFACE.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; X89102; CAA61474.1; -
CC EMBL; U08137; AAC50071.1; -
CC EMBL; U11821; AAC50124.1; -
CC EMBL; D38122; BAA07320.1; -
CC EMBL; Z96050; CAB09424.1; -
CC EMBL; AB013303; BAA32542.1; -
CC HSP; P01375; 2TUN.
CC MIM; 134638; -
CC InterPro; IPR000478; -
CC Pfam; PF00229; TNF; 1.
CC PROSITE; PS00251; TNF_1; 1.
CC PROSITE; PS50049; TNF_2; 1.
CC Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis.
CC DOMAIN 1 80
CC TRANSMEM 81 102
CC DOMAIN 103 281
CC DOMAIN 4 70
CC DOMAIN 45 65
CC DISULFID 202 233
CC CARBOHYD 184 184
CC CARBOHYD 250 250
CC CARBOHYD 260 260
CC SEQUENCE 281 AA; 31485 MW; A8A6EB358246E9BB CRC64;
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Query Match  
Best Local Similarity 7.0%; Score 87; DB 1; Length 281;  
Matches 50; Conservative 38; Mismatches 88; Indels 70; Gaps 11;

QY 14 PDPDPAWQVPGSVASPWSTPRMSTRSRYFYLLSTALVCLVAVAILLVVV----- 67  
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
DB 48 PPPPPPLPPPPLPPLPPLKRGN-----HSTGL-CLLVFMFVLVALVGLGLGM 101  
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
QY 68 -----OKKDSTNTTEKAPLKGNCSEDLFCILKTPSPSKSW---AYLQVSK 111  
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
DB 102 FQLFHLOKELAELRESTSQMHATSSLEKQIGHPS-----PPPERKEKLKVVAHLTKGS 153  
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
QY 112 HLANNTKLWNEDGTI---HGLTIQDGNLIYVFPGLYFIYVQLOFLVO---CSN----HSVDL 163  
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
DB 154 NSRSMPLWEPTYGIVLLSGVKYKKGLVINETGLYFVYSKYFRGSCNNLPUSHKV-- 211  
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
QY 164 TLQLLINSK-----IKKOFLVTVCESG-----VOSKNINYONLSQFLHY 202  
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
DB 212 ---YMRNSKYPQDLVMMEGKMMSYCTTGQMWARSYLGAVFNLTSADHLVYNVSELSLVN 268  
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
QY 203 LQVNST 208  
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
DB 269 FEESQT 274

RESULT 8  
TNFA\_MACMU STANDARD; PRG: 233 AA.  
ID TNFA\_MACMU AC P48094;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).  
GN TNF OR TNFA.  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96003435; PubMed=7561102;  
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;  
RT "Comparative sequence analysis of cytokine genes from human and nonhuman primates";  
RL J. Immunol. 155:3946-3954(1995).  
CC -! FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA. IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN CONDITIONS.  
CC -! SUBUNIT: HOMOTRIMER.  
CC -! SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM.  
CC -! PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTEOLYTIC PROCESSING.  
CC -! DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTIOUS, AND IS CHARACTERIZED BY GENERAL ILL HEALTH AND MALNUTRITION.  
CC -! SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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```
CC -----
DR EMBL; U23819; AAC49088.1; -.
KW SGP; S0006006; SEC16.
FT Mutagen 1058 1058 L->S: IN SEC16-4; TS ACCUMULATION OF ER
FT MUTAGEN 1083 1083 L->P: IN SEC16-3; TS ACCUMULATION OF ER
FT MUTAGEN 1088 1088 L->P: IN SEC16-2; TS ACCUMULATION OF ER
FT MUTAGEN 1230 1230 W->R: IN SEC16-1; TS ACCUMULATION OF ER
FT SEQUENCE 2194 AA; 241613 MW; BB1E02D2AD4683E3 CRC64;
SQ

Query Match 6.9%; Score 86.5; DB 1; Length 2194;
Best Local Similarity 20.9%; Pred. No. 12;
Matches 53; Conservative 39; Mismatches 87; Indels 75; Gaps 13;

QY 26 SVASPRWSTRP-----WRSTSRSYF-----YLTALVCLVVA 58
DB 969 SVAPPQRENPIKDNEALLRRQFFIFHWSAANKVVIYVPPIDQSQYMISSIVQEIKV 1028
QY 59 VAILVLVVOKKD---STPNTTEKAPLKGNGCEDLCTLKSTPSKKS-----WAYLOV 109
DB 1029 TPI--DQIKPNMMLKSPGPGLSAKLKKDKLTWKWETTKISSENESSDWTIMOLLEM 1086
QY 110 SKHLNKLWNEDGTHGLIYQDGNLIY-----QFGLY--FIVCQLQFL--VQ 155
DB 1087 KL---NDKVNKK---NISKLLYNSDELLMYLSQPPNGDMIPNAYRLDINCOMRVLAFLQ 1140
QY 156 CSNHVS-----DLTLQLLINSKIKQTLTVYC-----ESGVOSKNIYQNLSQLFLH 201
DB 1141 TGNHDEALRLALSCKRDYATALLVGLSGLMDRWSEVIQKLYEGFTAGPNDQKELAHFLL 1200
QY 202 YLOV---NSTISVR 212
DB 1201 IFQVFGVGNKMAIK 1214

RESULT 10
TN10_MOUSE
ID TN10_MOUSE STANDARD; PRT; 291 AA.
AC P50592;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 10 (TNF-RELATED
GN APOPTOSIS INDUCING LIGAND) (TRAIL PROTEIN).
OS TNFSF10 OR TRAIL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96111955; PubMed=8777713;
RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
RA Goodwin R.G.;
RT "Identification and characterization of a new member of the TNF
family that induces apoptosis.";
RL Immunity 3:673-682(1995).
CC -!- FUNCTION: INDUCES APOPTOSIS.
CC -!- SUBUNIT: HOMOTRIMER (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
CC -!- TISSUE SPECIFICITY: WIDESPREAD.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U37522; AAC52345.1; -.
DR MGD; MGI:107414; Tnfsf10.
DR InterPro; IPR000478; -.
DR Pfam; PF00229; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
KW Cytokine; Transmembrane; Signal-anchor; Apoptosis.
FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 39 291 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 52 52 N-LINKED (GLCNAC...)(POTENTIAL).
FT SEQUENCE 291 AA; 33477 MW; 3FEACAB9FD7D802 CRC64;
SQ

Query Match 6.8%; Score 85; DB 1; Length 291;
Best Local Similarity 21.2%; Pred. No. 1.3;
Matches 51; Conservative 34; Mismatches 94; Indels 62; Gaps 10;

QY 31 WRST-----RPWRSTSRSYFYLSTTALVCLVAVAI-----IIVLVQKKDSTPNTTEK 79
DB 69 WDSIDGELNRPCLQVAKQLYO-----LIEEVLRTFQDTISTVPERKQLSTP----- 115
QY 80 APLKGGNCSEDLCTLKSTPSKKSWAYLOVSKH---LNNTKLSWNEDGTHG-----LIYQ 132
DB 116 -PLPRGCRPKQVAAHITGITRRSSALIPISKDGKTLGQKIESWESSRKGHSFLNHLVR 174
QY 133 DGNLIYVFPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKQTLV----- 179
DB 175 NGELVIEQEGLYIYSQTYFRFQ-----EAEDASKMVSCKDKVTRKQLVQYIYKYTSYDPPI 230
QY 180 -----TVCEGVOSKNIYQNLSQLFLHYLVQNSTISVRVDFYVDYDTNFFLDNLSV 232
DB 231 VLKMSARNSCWSRDAEYGLY-SIYQGLFLKKNDRIFSVTNEHLM-----LDQEASF 284
QY 233 F 233
DB 285 F 285

RESULT 11
C307_DROME
ID C307_DROME STANDARD; PRT; 525 AA.
AC Q9VRM7;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROBABLE CYTOCHROME P450 307A1 (EC 1.14.-.-) (CYPCCCVI1A1).
GN CYP307A1 OR CG10594.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Cantier A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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Db 352 IQEIDAIIIEENSRINLLDNAMPYTNATIFEVLYRSS 391

RESULT 12
TNFB_MACEU
ID TNFB_MACEU STANDARD; PRT; 201 AA.
AC Q9XT48;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE LYMPHOTOXIN-ALPHA PRECURSOR (LT-ALPHA) (TNF-BETA).
LN LTA OR TNFB.
GN Macropus eugenii (Pammar wallaby).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315;
RN [1]
RP SEQUENCE FROM N.A.
RT Harrison G.A., Cooper D.W., Deane E.M.;
RT "cDNA cloning of lymphotoxin alpha (LT-a) from a marsupial, Macropus
RT eugenii."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases
CC -!- FUNCTION: LYMPHOTOXIN IS A CYTOKINE PRODUCED BY LYMPHOCYTES WHICH
CC IS CYTOTOXIC FOR A WIDE RANGE OF TUMOR CELLS IN VITRO AND IN VIVO.
CC -!- SUBUNIT: HETEROTRIMER OF EITHER TWO BETA AND ONE ALPHA SUBUNITS
CC OR (LESS PREVALENT) TWO ALPHA AND ONE BETA SUBUNITS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF119336; AAD41773.1; -
DR InterPro: IPR000478; -
DR InterPro: IPR002960; -
DR Pfam: PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCF.
DR PRINTS; PR01236; TNFBETA.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
DR Cytokine; Glycoprotein; Cytotoxin; Signal
DR SIGNAL 1 27 BY SIMILARITY.
DR CHAIN 28 201 LYMPHOTOXIN-ALPHA.
DR CARBOHYD 93 93 N-LINKED (GLCNAC. .) (POTENTIAL).
DR SEQUENCE 201 AA; 21536 MW; 8C4C371CB5091627 CRC64;

Query Match 6.7%; Score 83.5; DB 1; Length 201;
Best Local Similarity 22.3%; Pred. No. 1; 2;
Matches 49; Conservative 36; Mismatches 52; Indels 83; Gaps 14;

QY 47 LSTALVLCVAVAILVLVVQKQDSTPNTEKAPLKGNCSEDLCTLKSTPTSKKSWAY 106
Db 1 MTSSGVCLLGALSLQVLL-----QPPCAQAGAPNDNSH-----SSAPP---- 42
QY 107 LQYSKHLNNTKLS-----W--NEDGTI--HGLIYODGNLIVQFP 141
Db 43 -QTAQHLSSOKSLARETLKPAALHVGDPVSQVDSIHWRAANTDHATLRHGFSLSNNLSVPTS 101
QY 142 GLYFIVCQLOFL-VOQS-----NHSVDLTLQLLINSKIKQTILV-----TVCESGV 186
Db 102 GLYFVYSQVVFSGASCSEIPTLLLYLSHEV-----LLFSSKYQVHVPLLLSAQKSV- 155
QY 187 QS---KNIYQNLQSFLL-----HYLQVNSTI 209
Db 156 QGPWMSRVYOG-AVFLLITQGDRLSTYTDGVSHLLQSPSSV 194

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RESULT 13
TNFA_MACFA
ID TNFA_MACFA STANDARD; PRT; 233 AA.
AC P79337;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
GN TNF OR TNFA.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
RA Tatsumi M.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -!- SUBUNIT: HOMOTRIMER.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
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CC
CC EMBL; AB000513; BAA19131.1; -.
CC HSP; P01375; 1TNF.
CC InterPro: IPR000478; -.
CC InterPro: IPR002959; -.
CC Pfam: PF00229; TNF; 1.
CC PRINTS: PR01234; TNCRSISFCT.
CC PRINTS: PR01235; TNFALPHA.
CC PROSITE: PS00251; TNF_1; 1.
CC PROSITE: PS50049; TNF_2; 1.
CC Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
FT PROPEP 1 76 BY SIMILARITY.
FT CHAIN 77 233 TUMOR NECROSIS FACTOR.
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DISULFID 145 177 BY SIMILARITY.
SQ SEQUENCE 233 AA; 25558 MW; 6ABF2C3AB132C217 CRC64;

Query Match 6.7%; Score 83.5; DB 1; Length 233;
Best Local Similarity 23.4%; Pred. No. 1.4;
Matches 51; Conservative 40; Mismatches 100; Indels 27; Gaps 10;

Qy 19 AMQVPGSVASPRWTRPRWRSYFYLSTTA-LVCLVVAIVAILLVVQKKDSTPNNT 77
Dd 13 ABEALPRKTAGPQGRRCWFLSFLVAGATLFCLL-----HFGVIGPQREFFKDP 68
Qy 78 EKAPLKGNCSEDLCTLTKSTSKSWAYLOYSKHLNNTKLSW-NEDG---TIHGLIYQD 133
Dd 69 LISPLAQAVRSS-----SRTPSDKPAHV-VANPOAQGLQWLNRANVALVANGVELTD 121

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Qy 134 GNLIQFPGLYFIVCOLQFLVQ-CSNHSVDLT---LQLLINSKIKKQTLVTV---CE--- 183
Dd 122 NQLVVPSEGLYLIYSQVLFGQGCPSNNHVLVHTHTISIAVSYQTKVNLLSAISKPCQRET 181
Qy 184 -SGVQSKNIYQNLQSFLLHYLVQVNSTISVRVDFQYVD 220
Dd 182 PEGAEAPWYEPVILGVGFQLEKGRLSAEINLPDYLD 219

RESULT 14
TNFA_PAPHU
ID TNFA_PAPHU STANDARD; PRT; 233 AA.
AC O77510;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
GN TNF OR TNFA.
OS Papio hamadryas ursinus (Chacma baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Papio.
OX NCBI_TaxID=36229;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98147379; PubMed=9488055;
RA Haudek S.B., Redl H., Schlag G., Giroir B.P.;
RT "Complementary DNA (cDNA) sequence of baboon tumor necrosis factor
RT alpha.";
RL Mol. Immunol. 34:1041-1042(1997).
CC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -!- SUBUNIT: HOMOTRIMER.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC
CC EMBL; AF019963; AAC31675.1; -.
CC InterPro: IPR000478; -.
CC InterPro: IPR002959; -.
CC Pfam: PF00229; TNF; 1.
CC PRINTS: PR01234; TNCRSISFCT.
CC PRINTS: PR01235; TNFALPHA.
CC PROSITE: PS00251; TNF_1; 1.
CC PROSITE: PS50049; TNF_2; 1.
CC Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
FT PROPEP 1 76 BY SIMILARITY.
FT CHAIN 77 233 TUMOR NECROSIS FACTOR.
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DISULFID 145 177 BY SIMILARITY.
SQ SEQUENCE 233 AA; 25658 MW; B9403255058D4A03 CRC64;

Query Match 6.6%; Score 82.5; DB 1; Length 233;
Best Local Similarity 22.9%; Pred. No. 1.7;

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-----  
EMBL: U77083; AAB19065.1; --  
DR MEROPS; M01.001; --  
DR MGD; MGI:96749; Lap1.  
DR InterPro; IPR000130; --  
DR InterPro; IPR0001930; --  
DR Pfam; PF01433; Peptidase\_M1; 1.  
DR PRINTS; PR00756; ALADIPTASE.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
DR Hydrolase; Metalloprotease; Aminopeptidase; Zinc; Glycoprotein;  
KW Sulfatation; Transmembrane; Duplication; Signal-anchor.  
FT INIT\_MET 0 0 0 BY SIMILARITY.  
FT DOMAIN 1 7 CYTOPLASMIC.  
FT TRANSMEM 8 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
FT DOMAIN 32 67 CYTOSOLIC SER/THR-RICH JUNCTION.  
FT DOMAIN 68 965 METALLOPROTEASE.  
FT METAL 386 386 ZINC (CATALYTIC) (BY SIMILARITY).  
FT ACT\_SITE 387 387 BY SIMILARITY.  
FT METAL 390 390 ZINC (CATALYTIC) (BY SIMILARITY).  
FT

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2001, 10:21:50 ; Search time 31.97 Seconds  
(without alignments)  
569.463 Million cell updates/sec

Title: US-09-628-126-6  
Perfect score: 1246  
Sequence: 1 MEPLQAGSCGAPSPDPAM.....DTNTFPLDNVLSVFLYSSSD 239  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1246	100.0	239	2 B40710	CD30 ligand - mous
2	860.5	69.1	234	2 A40710	CD30 ligand - huma
3	123	9.9	279	2 A53062	Fas ligand - mouse
4	102	8.2	278	2 A45266	fas ligand - rat
5	91	7.3	309	2 I53384	4-lBB ligand - mou
6	89.5	7.2	235	2 I54490	tumor necrosis fac
7	89.5	7.2	401	2 S74767	hypothetical prote
8	87	7.0	281	2 I38707	Fas ligand - human
9	87	7.0	2013	2 C71610	probable membrane
10	86.5	6.9	2195	2 S61103	SEC16 protein - ye
11	86	6.9	674	2 S61181	hypothetical prote
12	85.5	6.9	994	2 H96510	probable disease r
13	84.5	6.8	884	2 T02731	serine/threonine-s
14	84	6.7	1110	2 F84547	probable disease r
15	83	6.7	889	2 T45691	receptor-like prot
16	82	6.6	234	1 JH0529	tumor necrosis fac
17	82	6.6	665	2 T05082	protein kinase hom
18	81.5	6.5	304	2 T27593	hypothetical prote
19	81.5	6.5	304	2 T27594	hypothetical prote
20	81	6.5	866	2 T10587	serine/threonine-s
21	81	6.5	890	2 C96654	hypothetical prote
22	80.5	6.5	344	2 T05104	hypothetical prote
23	80.5	6.5	663	2 H96533	hypothetical prote
24	80	6.4	165	2 H64460	hypothetical prote
25	80	6.4	369	2 S77028	protein kinase, 41
26	79.5	6.4	383	2 S67813	probable membrane
27	79.5	6.4	818	2 T02823	cell surface prote
28	79.5	6.4	1402	2 T17456	NUD1 protein - yea
29	79	6.3	851	2 S67285	

RESULT 1  
B40710  
CD30 ligand - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 05-Nov-1999  
C;Accession: B40710  
R;Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, Alderson, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, Cell 73, 1349-1360, 1993  
A;Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de  
A;Reference number: A40710; MUID:93313964  
A;Accession: B40710  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-239 <SMI>  
A;Cross-references: GB:L09754; NID:g349288; PIDN:AAA74595.1; PID:g349289  
C;Keywords: cytokine receptor; membrane protein; surface antigen

Query Match 100.0%; Score 1246; DB 2; Length 239;  
Best Local Similarity 100.0%; Pred. No. 6.4e-106;  
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPLQAGSCGAPSPDPAMQVPGSVASVAPWRSRSTPRWSTSRSYFLSTALVCLVAVA 60  
Db 1 MEPLQAGSCGAPSPDPAMQVPGSVASVAPWRSRSTPRWSTSRSYFLSTALVCLVAVA 60  
Qy 61 IILVLVQKDSPTNTTEKAPLKGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSW 120  
Db 61 IILVLVQKDSPTNTTEKAPLKGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSW 120  
Qy 121 NEDGTIHLIYODGNLIYVFCGLYFVCOLOFLVOCNSHSDTLTQLLINSKIKQTIVT 180  
Db 121 NEDGTIHLIYODGNLIYVFCGLYFVCOLOFLVOCNSHSDTLTQLLINSKIKQTIVT 180  
Qy 181 VCESGVQSKNIYQNLSQLFLHYLVQNSITSVRVDFNQVDTNTFFLDNVLSVFLYSSSD 239  
Db 181 VCESGVQSKNIYQNLSQLFLHYLVQNSITSVRVDFNQVDTNTFFLDNVLSVFLYSSSD 239

RESULT 2  
A40710  
CD30 ligand - human  
C;Species: Homo sapiens (man)  
C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 21-Jul-2000  
C;Accession: A40710  
R;Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, Alderson, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, Cell 73, 1349-1360, 1993  
A;Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de  
A;Reference number: A40710; MUID:93313964  
A;Accession: A40710

ALIGNMENTS

2

[illegible]







Db 102 FOLFHLQKELARESTSQMHTASSLEKQIGHPS-----PPPEKKELRKVAHITGKS 153  
Qy 112 HLNNTKLSWNEGTI---HGLIYQDGNLIVFPGLFYIVCQQLVQ-CSN-----HSVDL 163  
Db 154 NSRSPLEWEDYIGVLLSGVYKKGGLVNETGLYFVYSKYVFGQSCNNLPSHKV-- 211  
Qy 164 TLQLLINSK-----IKKQTLVTVCESG-----VQSKNIYQNLISQFLHY 202  
Db 212 ---YMRNSKYPQDLVMECKMMSYCTTGOMWARSSYLGAVENTLSADHLVYVNSLSLVN 268  
Qy 203 LQVNST 208  
Db 269 FEESQT 274  
RESULT 9  
C71610  
probable membrane associated protein PFB0615c - malaria parasite (Plasmodium falciparum)  
C:Species: Plasmodium falciparum  
C:Date: 13-Nov-1998 #sequence\_revision 13-Nov-1998 #text\_change 21-Jul-2000  
C:Accession: C71610  
R:Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;  
Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.;  
Science 282, 1126-1132, 1998  
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.  
A:Reference number: A71600; MUID:99021743  
A:Accession: C71610  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-2013 <GAR>  
A:Cross-references: GB:AE001406; GB:AE001362; NID:g3845230; PIDN:AAC71912.1; PID:g384523  
A:Experimental source: clone 3D7  
C:Genetics:  
A:Gene: PFB0615c  
Query Match 7.0%; Score 87; DB 2; Length 2013;  
Best Local Similarity 23.9%; Pred. No. 22;  
Matches 34; Conservative 31; Mismatches 49; Indels 28; Gaps 7;  
Qy 88 SEDLFTLKSTPSKSWAYLQVSKHLNWKLSWNEGTTHGLIYQDGNLIVFPGLFYIV 147  
Db 16 SDNIFCFLKD-----GYICFMNLLN-----NEKKVLYIFCSQDEGYVAQY---YFDV 59  
Qy 148 COLOFLVQCSNHSVDLTQLLI-----NSKIKKQTLVTVCESGVQSKNIYQNLISQFL-- 200  
Db 60 VKCRYEKKEDCNKMTINIMLLQNNKKIKETCYI---KNVVTNKIYHTL--FLVINK 114  
Qy 201 HYLVQNSTISVRVDNFOYVDN 222  
Db 115 HYHNILCSLSPENNSFEILTNTN 136  
RESULT 10  
S61103  
SEC16 protein - yeast (Saccharomyces cerevisiae)  
N:Alternate names: protein Lpf1w; protein YPL085w  
C:Species: Saccharomyces cerevisiae  
C:Date: 23-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 06-Feb-1998  
C:Accession: S61103  
R:Hall, J.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.; Vo, D.H.; wa  
submitted to the EMBL Data Library, August 1995  
A:Description: The sequence of Saccharomyces cerevisiae  
A:Reference number: S59677  
A:Accession: S61103  
A:Molecule type: DNA  
A:Residues: 1-2195 <HAL>  
A:Cross-references: EMBL:U41849; NID:g1147608; PID:g1147609; MIPS:YPL085w  
C:Genetics:  
A:Gene: SGD:SEC16  
A:Cross-references: SGD:S0006006; MIPS:YPL085w  
A:Map position: 16L  
C:Keywords: transmembrane protein

F:1198-1214/Domain: transmembrane #status predicted <TM1>  
F:1250-1266/Domain: transmembrane #status predicted <TM2>

Query Match 6.9%; Score 86.5; DB 2; Length 2195;  
Best Local Similarity 20.9%; Pred. No. 27;  
Matches 53; Conservative 39; Mismatches 87; Indels 75; Gaps 13;

Qy 26 SVASPPWSTRP-----WRSTSRSYF-----YLTSTALVCLVVA 58

Db 970 SVAPPQRENPIKIDNEALLRQFPFPHWSANKVYAVPIPPDQSQYMISSIVQEIKV 1029

Qy 59 VAILVLVQKKD---STPNTEKAPLKGGNCSEDLCTLKSTPSKKS-----WAYLQV 109

Db 1030 TPI--DQIIKPNMDLKSFGPGLGSAKKKDLTKWMTTIKSIENESSTDMTIWQLLE 1087

Qy 110 SKHLNWKLSWNEGTTHGLIYQDGNLIV-----QPPGLY--FIVCQQLF--VQ 155

Db 1088 KL---NDKVNWK---NISKLLYNSDELLMYLSQPPFGDMIPNAYRLDINQMRVLAFLQ 1141

Qy 156 CSNHSV-----DLTLQLLINSKIKKQTLVTVC-----ESGVQSKNIYQNLISQFLH 201

Db 1142 TGNHDEALRLALSARDYAIALLVGLSLGKDRWSEVIQKLYEGFTAGPDNOKELAHFLLL 1201

Qy 202 YLQV---NSTISVR 212

Db 1202 IFQVFGNSKMAIK 1215

RESULT 11

S61181

hypothetical protein YDR295c - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein D9740.10

C:Species: Saccharomyces cerevisiae

C:Date: 23-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 23-Mar-2001

C:Accession: S61181

R:Ding, H.

submitted to the EMBL Data Library, June 1995

A:Description: The sequence of S. cerevisiae cosmid 9740.

A:Reference number: S61160

A:Accession: S61181

A:Molecule type: DNA

A:Residues: 1-674 <DIN>

A:Cross-references: EMBL:U28374; NID:g849207; PID:g849217; GSPDB:GN00004; MIPS:YDR295

C:Genetics:

A:Gene: MIPS:YDR295c

A:Map position: 4R

Query Match 6.9%; Score 86; DB 2; Length 674;  
Best Local Similarity 25.0%; Pred. No. 7.1;  
Matches 40; Conservative 30; Mismatches 60; Indels 30; Gaps 9;

Qy 70 KDSTPNTEKAPLKGGNCSEDLCTLKSTPSKK-----SWAYLQVSKHLNNTK- 117

Db 192 KDGTPTSVSSTSSNSNSTSYTGSKDDYDYSVRNLKRRKINTDDMLFLATTKLKHQDY 251

Qy 118 LSWNEGTTHGLIYQDGNLIVFPGLFYI-----VCLOFLVQCSNHSVDLTQLLIN 170

Db 252 LLANYD--IDMIISFDPMLEVPALQVLRNNAKNDPIIKLLVQ---NSPND---HYLLD 303

Qy 171 SKTKKQTLVT--VCESG-VQSKNIYQNLISQFLHYLQVNS 207

Db 304 SEIKNSVSKSHLSNNGHVDDSQEYBEIKSSLLYFLQARN 343

RESULT 12

H96510

probable disease resistance protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C:Accession: H96510

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719  
A:Accession: H96510  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-994 <STO>  
A:Cross-references: GB:AE005173; NID:g11321768; PIDN:AAC34245.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: F2G19.6  
A:Map position: 1

Query Match 6.9%; Score 85.5; DB 2; Length 994;  
Best Local Similarity 26.3%; Pred. No. 13;  
Matches 40; Conservative 21; Mismatches 64; Indels 27; Gaps 8;  
QY 107 LQVSKHLNNTKLSWNE-DGTIHLI-----YQDGNLIVQFGLYFIVCLOFLVQ 155  
Db 322 LRSLSHLNVLSENNFVEIPSSVNLKQLTLDVSDNNLNGFSSLLNLNQLRVIDI 381  
QY 156 CSNHSVDLTQLLINSKIRKQTIVTVCSGVQSK-----NIYQNLSQFLHLVQVNSTI 209  
Db 382 CSNHFTGLPPIT--SOLSNLEFFSACDSFTGISPSLFINI--SSLTGLSLYNQLNDTT 438  
QY 210 SVR----VDNFQ--YVDNTTFPLDNY-LSVFL 234  
Db 439 NIKNTSLHLNQLRLDNNFRASQVDLDVFL 470

RESULT 13  
T02731  
serine/threonine-specific protein kinase (EC 2.7.1.1) T9I4.7 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 16-Feb-2001  
C:Accession: T02731; D84691  
R:Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M.; Ron  
submitted to the EMBL Data Library, August 1998  
A:Description: Arabidopsis thaliana chromosome II BAC T9I4 genomic sequence.  
A:Reference number: Z14710  
A:Accession: T02731  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-884 <ROU>  
A:Cross-references: EMBL:AC005315; NID:g3461834; PIDN:AAC33227.1; PID:g3461841; GSPDB:GN  
A:Experimental source: cultivar Columbia  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487  
A:Accession: D84691  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-884 <STO>  
A:Cross-references: GB:AE002093; NID:g3461841; PIDN:AAC33227.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: ATSP:T9I4.7; At2g28990  
A:Map position: 2  
A:Introns: 24/1; 203/2; 362/1; 410/2; 434/2; 458/2; 484/2; 538/1; 621/3; 664/1; 686/1; 7  
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol  
C:Keywords: phosphotransferase; protein kinase

Query Match 6.8%; Score 84.5; DB 2; Length 884;

Best Local Similarity 25.1%; Pred. No. 14;  
Matches 52; Conservative 28; Mismatches 76; Indels 51; Gaps 12;  
QY 48 STTALVCLVAVAILLVVQVKDSTPNTTEKAPL-----KGGNC-SDLEFCTTKSPSK 101  
Db 512 SAASLVIVVVVA--LFFVFRKKASPSNLHAPPSPVSPNPGHNSQSESSF-----TSKK 564  
QY 102 KSWAYLQVSKHLNNTKLSWNE-DG---TIHGLIYQDGNLIVQFGLYFIVCLOFLVQCSN 158  
Db 565 IRFTYSEVQEQNTNFDKALGEGFGVYVHGFV---NVIEQ-----VAVKLLSOSSS 612  
QY 159 H-----SVDLTQLLINSKIRKQTIVTVCSGVQSKNIYQ-----NLSQFL-----H 201  
Db 613 QGYKHFAEVELLMRV---HHNLVSLVGYCDEGEHLALIYEYMPNGDLKQHLKSKHGCF 669  
QY 202 YLQVNSTISVRD---NFQYVDVNTFF 225  
Db 670 VLSWESRLKIVLDAALGLELYLHTGCV 696

RESULT 14  
F84547  
probable disease resistance protein [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C:Accession: F84547  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487  
A:Accession: F84547  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1110 <STO>  
A:Cross-references: GB:AE002093; NID:g6598362; PIDN:AAF18600.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g17060  
A:Map position: 2

Query Match 6.7%; Score 84; DB 2; Length 1110;  
Best Local Similarity 22.7%; Pred. No. 20;  
Matches 44; Conservative 36; Mismatches 66; Indels 48; Gaps 10;  
QY 46 YLSTALVCLVAV---AIIIV-----LVVQKDSPTNTERKAPLKGKNCSEDLFCTL 95  
Db 680 YLQGTAKRCPTSTENLQKLLLDLKCEVLSPLDCLGNLRSIQELILSGCSK-----L 734  
QY 96 KSTPSKSWAYLQVSKHLNNTKLSWNE-DGTHGLIYQDGNLIVQFGLYFIVCLOFLVQ 155  
Db 735 KFFPELK-----ETMKSIK-----ILLDGTAKOMPIL--LQC-----IQ 768  
QY 156 CSNHSV-DLTQLLINSKIRKQTIVTVCSGVQSKNIYQNLSQ-FLHLYQVNS-----T 208  
Db 769 SQGHSVANKTLPNSLDYILPSSLLSLCLSGNDIESLHANISQLYHLKWLDKNCKKLKS 828  
QY 209 ISVRVDNFQYVDN 222  
Db 829 VSVLPPLNKLCLDAH 842

RESULT 15  
T45691  
receptor-like protein kinase homolog - Arabidopsis thaliana  
N:Alternate names: protein F18L15.60  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 04-Mar-2000  
C:Accession: T45691  
R:Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.;  
submitted to the Protein Sequence Database, November 1999  
A:Reference number: Z23010

Search completed: September 5, 2001, 10:23:51  
Job time: 121 sec

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	181.5	14.6	95	5	US-09-758-468-439	Sequence 439, App
2	119	9.6	55	1	PCT-US01-08656-9656	Sequence 9656, Ap
3	102	8.2	278	1	PCT-US01-21282-6	Sequence 6, Appli
4	102	8.1	278	5	US-09-899-059-6	Sequence 6, Appli
5	83.5	6.7	362	5	US-09-764-853-532	Sequence 532, App
6	83.5	6.7	523	1	PCT-US01-10472-300	Sequence 300, App
7	80.5	6.5	233	1	PCT-US01-21282-3	Sequence 3, Appli
8	80.5	6.5	233	5	US-09-879-919-5	Sequence 5, Appli
9	80.5	6.5	233	5	US-09-899-059-3	Sequence 3, Appli
10	79	6.3	350	1	PCT-US01-16450-2513	Sequence 2513, Ap
11	79	6.3	360	5	US-09-758-472-8446	Sequence 8446, Ap
12	78.5	6.3	271	1	PCT-US01-16450-2658	Sequence 2658, Ap
13	78	6.3	347	1	PCT-US01-14827-10562	Sequence 10562, A
14	78	6.3	391	5	US-09-813-398-24	Sequence 24, Appli
15	78	6.3	426	5	US-09-868-604-8	Sequence 8, Appli
16	76.5	6.1	251	1	PCT-US01-21282-20	Sequence 20, Appli
17	76.5	6.1	251	5	US-09-899-059-20	Sequence 20, Appli
18	76.5	6.1	317	5	US-09-577-780-13	Sequence 13, Appli
19	76	6.1	2367	1	PCT-US01-14827-9813	Sequence 9813, Ap
20	75	6.0	424	1	PCT-US01-16450-2690	Sequence 2690, Ap
21	75	6.0	1014	1	PCT-US01-14827-14206	Sequence 14206, A
22	74.5	6.0	198	5	US-09-738-626-4749	Sequence 4749, Ap
23	74.5	6.0	238	5	US-09-839-894-2	Sequence 2, Appli
24	74.5	6.0	1103	5	US-09-570-581A-1840	Sequence 1840, Ap
25	74.5	6.0	1103	5	US-09-573-655A-338	Sequence 338, App
26	74.5	6.0	1103	5	US-09-573-655A-656	Sequence 656, App
27	73.5	5.9	309	1	PCT-US01-10739-8	Sequence 8, Appli

```

> AFFILIATION: HYSEQ, LLC
> TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
> FILE REFERENCE: 21272-066
> CURRENT APPLICATION NUMBER: PCT/US01/08656
> CURRENT FILING DATE: 2001-04-16
> PRIOR APPLICATION NUMBER: 09/522,929
> PRIOR FILING DATE: 2000-04-18
>

```





```

Query Match      6.3%   Score 79; DB 1; Length 350;
Best Local Similarity 25.3%; Pred. No. 8.4;
Matches 40; Conservative 25; Mismatches 55; Indels 38; Gaps 7;

QY       51 ALVCLVVAVAI-----ILVLVOKKDS-----TPNTEKAPLKGNCSED 90
    || :|||:||:          :|||:||:         :|||:||:         :|||:||:
DB      167 AILHLVSLAMHFRAPIRLPEHVTVQVVVKRGLLHSSHISELTITTEMNGRFERD 226

QY       91 LFCTL-----KSTPSKKSWAYLOVSKHLNNTKLSWNEDGTIHGILIYODGNLIIVQFGL- 143
    || | ||| | -||| | -||| | -||| | -||| | -||| | -||| |
DB      227 AFDTLFDAHPDKLSVVRKSLTF-VNKHLKNLEVELETE----QFADGYVLVLLMGLL 281

QY      144 --VFIVCQLFVQCS----NHSVDLTQLQLINSKIRK 175
    || | | | | | | | | | | | | | | | | | | | | | | | |
DB      282 EDYFVPLHHLYLPESFDQKVHNVSFAFELMLDGCLKK 319


RESULT 11
US-09-758-472-8446
; Sequence 8446, Application US/09758472
GENERAL INFORMATION:
```

```

QY   69 KKDST---PNTTEKAPLKGGNCSEDLFCTIKSTPSKKSWAYLQVSKHLNNTKLWSNEDGT 124
    |      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   137 KSMTEFGPDVKKKTEDEVEDCDLLIACQPESSLKALDF-EVSE--ARTEVEVEELPP 193
    |      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY   126 I-HGLIYODGNLIYVOFPCLYFIVCOLQFLVOCNSHSDVLTLOLLLSKI----- 173
    | ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   194 IDHGIPITDRRSTEQ-AHLAPVVCPOKVKGMLS-----KLVENKKIASATHNIYAYR 219
    | ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY   174 ----KKOTLVTCVCSGSGKNINYQLSOFLLHYLQVNSTISVRV-----DNFYVV 219
    | ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   245 IYCEDIKQTFLQDCED--DGETVAGGRLLHLMELLVSVDVMGVRARWYVGMGLGDPDKHI 302
    |      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY   220 DTTNFPLDNLVSLEYSSS 238
    :      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   303 NN---CVRNILVENKYTSS 318
    :      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 14
US-09-813-398-24
; Sequence 24, Application US/09813398
; GENERAL INFORMATION:
; APPLICANT: Bruce D. Weintraub
; APPLICANT: Mariusz W. Szkuclinski
; APPLICANT: University of Maryland
; TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
; FILE REFERENCE: UOPMD.003C1
; CURRENT APPLICATION NUMBER: US/09/813,398
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: PCT/US99/05908
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/US98/19772
; PRIOR FILING DATE: 1998-09-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 397
; TYPE: PR
; ORGANISM: HOMO SAPIEN
```



US-09-813-398-24

```
Query Match          6.3%; Score 78; DB 5; Length 397;
Best Local Similarity 18.5%; Pred No. 12;
Matches 59; Conservative 43; Mismatches 93; Indels 124; Gaps 12;

QY 6 0OAGSCGAPSPDPAMQVQSGVSPWRSTRPWR-----TSRSFYFLSTTALVCL 55
Db 86 RHSGQPGSPADPHRLR-RAASRANTVRSFPHHEESLEELPETSCKTTRFFFNLSIPTEE 144
QY 56 VVAIAIILVIVQKDDSTPNTT-----EKAP-----LKGNCSE 89
Db 145 FITSAELQVFEQMDALGNNSFHRINIYEIKPATANSKFPVTRLLDTRLVNQNASR 204
QY 90 DLFTCLKSTPSKSWA-----YLOVSKHLNNTKLSWNE-- 122
Db 205 --WESFDVTPAVMRWTAQGHANHGFWVEVAHLEEKQGVSKRHRVRSLSLHQDEHSWSQIR 262
QY 123 -----DGTIHL-----IYQD-----GNLIVQFPGLY 144
Db 263 PLLVTFHGDGKGPLHKKREKQAKQKRLKSSCKRHPLYVDFSDVGWMDWIVAPPGVH 322
QY 145 FIVCQ-----LQFLVQCSNHSVDLTLQLLINSKIKKQTLVTVCESGVOSKNIYQNLQSF 198
Db 323 AFYCHGECPPFLADHLNSTHAIQVTLVNSVNSKIPKACCVPT-----ELSAI 370
QY 199 LLHYLVQNVNSTISVRVDNFQ 217
Db 371 SMLYLDENEKVVLK--NIQ 387
```

```
RESULT 15
US-09-868-604-8
; Sequence 8, Application US/09868604
; GENERAL INFORMATION:
; APPLICANT: Alex Bollen
; APPLICANT: Alain Fauconnier
; APPLICANT: Edmond Godfroid
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45168
; CURRENT APPLICATION NUMBER: US/09/868.604
; CURRENT FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Bordetella pertussis
US-09-868-604-8
```

```
Query Match          6.3%; Score 78; DB 5; Length 426;
Best Local Similarity 32.4%; Pred. No. 13;
Matches 24; Conservative 8; Mismatches 40; Indels 2; Gaps 2;

QY 11 CGAPSPDPAMQVQSGVSP-WRSTRPWRSTRSYFYFLSTTALVCLV-VVAIAIILVIVQ 68
Db 104 CGPDGSDTALHDVPGSTSPSPSVAALMPRRRAGRPWLALGAAAVLLVGLATALVSVTTTPA 163
QY 69 KDDSTPNTTEKAPL 82
Db 164 TPAAPPTPTAPL 177
```

Search completed: September 5, 2001, 10:28:27  
Job time: 397 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2001, 10:21:45 ; Search time 25.09 Seconds  
(without alignments)  
196.138 Million cell updates/sec

Title: US-09-628-126-6  
Perfect score: 1246  
Sequence: 1 MEPLQAGSCGAPSPDPAM.....DTNFTPLDNLVSLYSSD 239

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1246	100.0	239	1	US-08-225-989-6
2	1246	100.0	239	1	US-08-570-923-6
3	1246	100.0	239	1	US-08-580-014-6
4	1246	100.0	239	4	US-09-079-785-6
5	1141	91.6	220	1	US-08-225-989-19
6	1141	91.6	220	1	US-08-570-923-19
7	1141	91.6	220	1	US-08-580-014-19
8	1141	91.6	220	4	US-09-079-785-19
9	860.5	69.1	234	1	US-08-225-989-8
10	860.5	69.1	234	1	US-08-570-923-8
11	860.5	69.1	234	1	US-08-580-014-8
12	860.5	69.1	234	4	US-09-079-785-8
13	814.5	65.4	215	1	US-08-225-989-23
14	814.5	65.4	215	1	US-08-570-923-23
15	814.5	65.4	215	1	US-08-580-014-23
16	814.5	65.4	215	4	US-09-079-785-23
17	685	55.0	130	1	US-08-225-989-21
18	685	55.0	130	1	US-08-570-923-21
19	685	55.0	130	1	US-08-580-014-21
20	685	55.0	130	4	US-09-079-785-21
21	624	50.1	148	3	US-08-584-031-12
22	391.5	31.4	125	1	US-08-225-989-20
23	391.5	31.4	125	1	US-08-570-923-20
24	391.5	31.4	125	1	US-08-580-014-20
25	391.5	31.4	125	4	US-09-079-785-20
26	229	18.4	52	4	US-09-369-494-17
27	115	9.2	279	5	PCT-US95-00362-5

28	91	7.3	309	1	US-08-236-918A-2	Sequence 2, Appli
29	87	7.0	281	2	US-08-810-453-2	Sequence 2, Appli
30	87	7.0	281	3	US-08-815-190A-2	Sequence 2, Appli
31	87	7.0	281	4	US-09-290-640-25	Sequence 25, Appli
32	87	7.0	281	4	US-09-479-524-3	Sequence 3, Appli
33	87	7.0	281	5	PCT-US95-00362-2	Sequence 2, Appli
34	85	6.8	291	1	US-08-670-354-6	Sequence 6, Appli
35	85	6.8	291	5	PCT-US96-10895-6	Sequence 6, Appli
36	83.5	6.7	287	3	US-08-815-190A-16	Sequence 16, Appli
37	83	6.7	550	2	US-08-417-210A-140	Sequence 140, App
38	83	6.7	551	2	US-08-417-210A-137	Sequence 137, App
39	83	6.7	551	2	US-08-417-210A-143	Sequence 143, App
40	83	6.7	857	1	US-08-022-835-4	Sequence 4, Appli
41	83	6.7	857	1	US-08-388-809-4	Sequence 4, Appli
42	83	6.7	857	2	US-08-647-714-4	Sequence 8, Appli
43	82.5	6.6	183	4	US-09-105-343A-8	Sequence 2, Appli
44	82	6.6	396	2	US-07-989-847-2	Sequence 2, Appli
45	82	6.6	396	4	US-08-469-411-2	Sequence 2, Appli

#### ALIGNMENTS

RESULT 1  
US-08-225-989-6  
; Sequence 6, Application US/08225989  
; Patent No. 5480981  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-570-923-6

Query Match 100.0%; Score 1246; DB 1: Length 239;
Best Local Similarity 100.0%; Pred. No. 1.2e-116;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPGLQAGSCGAPSPDPAMQVPGSVASPMWRSTPRWRSTSRSYFYLTALVCLVVAVA 60
Db 1 MEPGLQAGSCGAPSPDPAMQVPGSVASPMWRSTPRWRSTSRSYFYLTALVCLVVAVA 60
Qy 61 IILVLVQKKDSTNTTEKAPLKGNCSEDLFCTLKSTPSKKSWAYLOVSKHLNNTKLSW 120
Db 61 IILVLVQKKDSTNTTEKAPLKGNCSEDLFCTLKSTPSKKSWAYLOVSKHLNNTKLSW 120
Qy 121 NEDGTIIGLIYQDGNLIVPFGLYFIVCOLQFLVQCSNHSVDLTLQLLINSIKKKQTLVT 180
Db 121 NEDGTIIGLIYQDGNLIVPFGLYFIVCOLQFLVQCSNHSVDLTLQLLINSIKKKQTLVT 180
Qy 181 VCESGVQSKNIYQNLQSOFLHLHYLOVNSTISVRVDNFQYVDNTFPLDNVLSVFLYSSD 239
Db 181 VCESGVQSKNIYQNLQSOFLHLHYLOVNSTISVRVDNFQYVDNTFPLDNVLSVFLYSSD 239

RESULT 3
US-08-580-014-6
; Sequence 6, Application US/08580014
; Patent No. 5753203
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,014
; FILING DATE: 20-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992

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CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-580-014-6

Query Match 100.0%; Score 1246; DB 1; Length 239;  
Best Local Similarity 100.0%; Pred. No. 1.2e-116;  
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MEPGLQAGSCGAPSPDPAMQVPGSVASPRWSTSRYSFYLTALVCLVAVA 60  
Db 1 MEPGLQAGSCGAPSPDPAMQVPGSVASPRWSTSRYSFYLTALVCLVAVA 60  
Qy 61 IILVLVQKKDSTPNTTEKAPLKGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSW 120  
Db 61 IILVLVQKKDSTPNTTEKAPLKGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSW 120  
Qy 121 NEDGTIHLIYQDGNLIVQFPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLVT 180  
Db 121 NEDGTIHLIYQDGNLIVQFPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLVT 180  
Qy 181 VCESGVQSKNIYQNLSQFLHLYQVNSTISVRVDNFQYVDNTFPDLNVLVSFLYSSSD 239  
Db 181 VCESGVQSKNIYQNLSQFLHLYQVNSTISVRVDNFQYVDNTFPDLNVLVSFLYSSSD 239

RESULT 4  
US-09-079-785-6  
Sequence 6, Application US/09079785  
Patent No. 6143869  
GENERAL INFORMATION:  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
APPLICANT: Armitage, Richard J.  
APPLICANT: Gruss, Hans-Jurgen  
TITLE OF INVENTION: No. 6143869el Cytokine That Binds CD30  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1

SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,785  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,989  
FILING DATE: 12 APRIL 1994  
APPLICATION NUMBER: US 07/966,775  
FILING DATE: 27-OCT-1992  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-079-785-6

Query Match 100.0%; Score 1246; DB 4; Length 239;  
Best Local Similarity 100.0%; Pred. No. 1.2e-116;  
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MEPGLQAGSCGAPSPDPAMQVPGSVASPRWSTSRYSFYLTALVCLVAVA 60  
Db 1 MEPGLQAGSCGAPSPDPAMQVPGSVASPRWSTSRYSFYLTALVCLVAVA 60  
Qy 61 IILVLVQKKDSTPNTTEKAPLKGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSW 120  
Db 61 IILVLVQKKDSTPNTTEKAPLKGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSW 120  
Qy 121 NEDGTIHLIYQDGNLIVQFPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLVT 180  
Db 121 NEDGTIHLIYQDGNLIVQFPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLVT 180  
Qy 181 VCESGVQSKNIYQNLSQFLHLYQVNSTISVRVDNFQYVDNTFPDLNVLVSFLYSSSD 239  
Db 181 VCESGVQSKNIYQNLSQFLHLYQVNSTISVRVDNFQYVDNTFPDLNVLVSFLYSSSD 239

RESULT 5  
US-08-225-989-19  
Sequence 19, Application US/08225989  
Patent No. 5480981  
GENERAL INFORMATION:  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
APPLICANT: Armitage, Richard J.  
APPLICANT: Gruss, Hans-Jurgen  
TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,989  
FILING DATE: 12 APRIL 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/966,775  
FILING DATE: 27-OCT-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 220 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-225-989-19

Query Match 91.6%; Score 1141; DB 1; Length 220;  
Best Local Similarity 100.0%; Pred. No. 3.2e-106;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 MOVQPGSVASPRWSTSRSYFYLTALVCLVAVAILLVVQKDKSTPNTTEK 79  
Db 1 MOVQPGSVASPRWSTSRSYFYLTALVCLVAVAILLVVQKDKSTPNTTEK 60  
QY 80 APLKGGNCSEDLFTCLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQV 139  
Db 61 APLKGGNCSEDLFTCLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQV 120  
QY 140 FPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQFLVTVCSGVQSKNIYQNLSQL 199  
Db 121 FPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQFLVTVCSGVQSKNIYQNLSQL 180  
QY 200 LHYLVNSTISVRVDNQYVDTNFFPLDNVLSVLYSSD 239  
Db 181 LHYLVNSTISVRVDNQYVDTNFFPLDNVLSVLYSSD 220

RESULT 6  
US-08-570-923-19  
; Sequence 19, Application US/08570923  
; Patent No. 5677430

GENERAL INFORMATION:  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
APPLICANT: Armitage, Richard J.  
APPLICANT: Gruss, Hans-Jurgen  
TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/570,923  
FILING DATE: 12-DEC-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,989  
FILING DATE: 12 APRIL 1994  
APPLICATION NUMBER: US 07/966,775  
FILING DATE: 27-OCT-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 220 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-570-923-19

Query Match 91.6%; Score 1141; DB 1; Length 220;  
Best Local Similarity 100.0%; Pred. No. 3.2e-106;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 MOVQPGSVASPRWSTSRSYFYLTALVCLVAVAILLVVQKDKSTPNTTEK 79  
Db 1 MOVQPGSVASPRWSTSRSYFYLTALVCLVAVAILLVVQKDKSTPNTTEK 60  
QY 80 APLKGGNCSEDLFTCLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQV 139  
Db 61 APLKGGNCSEDLFTCLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQV 120  
QY 140 FPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQFLVTVCSGVQSKNIYQNLSQL 199  
Db 121 FPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQFLVTVCSGVQSKNIYQNLSQL 180

QY 200 LHYLOVNSTISVRVDFQYVDTNTFPDLNVLVSFLYSSSD 239  
Db 181 LHYLOVNSTISVRVDFQYVDTNTFPDLNVLVSFLYSSSD 220

## RESULT 7

US-08-580-014-19  
; Sequence 19, Application US/08580014  
; Patent No. 5753203  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/580,014  
; FILING DATE: 20-DEC-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 220 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-580-014-19

Query Match 91.6%; Score 1141; DB 1; Length 220;  
Best Local Similarity 100.0%; Pred. No. 3.2e-106;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 MQVQPGSVASPRSTRPWRSTSRSYFLSTALVCLVAVAILLVVQKDKSTPNTTEK 79

Db 1 MQVQPGSVASPRSTRPWRSTSRSYFLSTALVCLVAVAILLVVQKDKSTPNTTEK 60  
QY 80 APLKGGNCSEDLFCTLKSTPKSKSWAYLQVSKHLNNTKLSWNEDGTIHLGLIYQDGNLIQV 139  
Db 61 APLKGGNCSEDLFCTLKSTPKSKSWAYLQVSKHLNNTKLSWNEDGTIHLGLIYQDGNLIQV 120  
QY 140 FPGLYFIVCQLQFLVQCSNHSVDLTLQLLINSKIKKQTLVTVCESGVQSKNIYONLSQFL 199  
Db 121 FPGLYFIVCQLQFLVQCSNHSVDLTLQLLINSKIKKQTLVTVCESGVQSKNIYONLSQFL 180  
QY 200 LHYLOVNSTISVRVDFQYVDTNTFPDLNVLVSFLYSSSD 239  
Db 181 LHYLOVNSTISVRVDFQYVDTNTFPDLNVLVSFLYSSSD 220

## RESULT 8

US-09-079-785-19  
; Sequence 19, Application US/09079785  
; Patent No. 6143869  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 6143869el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/079,785  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 220 amino acids  
; TYPE: amino acid

; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-079-785-19

Query Match 91.6%; Score 1141; DB 4; Length 220;  
Best Local Similarity 100.0%; Pred. No. 3.2e-106;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 MQVQGSVSPWRSTPRWSTSRSYFLSTALVCLVAVAILLVVQKDKSTPNTTEK 79  
Db 1 MQVQGSVSPWRSTPRWSTSRSYFLSTALVCLVAVAILLVVQKDKSTPNTTEK 60  
Qy 80 APLKGCNSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHLIYQDGNLIQV 139  
Db 61 APLKGCNSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHLIYQDGNLIQV 120  
Qy 140 FPLGLFIYVQQLQFLVQCSNHSVDLTQLLINSKIKKQTLVTVCSGVQSKNIYQNSQFL 199  
Db 121 FPLGLFIYVQQLQFLVQCSNHSVDLTQLLINSKIKKQTLVTVCSGVQSKNIYQNSQFL 180  
Qy 200 LHYLVNSTISVRVDFQVDTNTPFLDNVLSVFLYSSSD 239  
Db 181 LHYLVNSTISVRVDFQVDTNTPFLDNVLSVFLYSSSD 220

## RESULT 9

US-08-225-989-8  
; Sequence 8, Application US/08225989  
; Patent No. 5480981  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,989  
FILING DATE: 12 APRIL 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 234 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-225-989-8

Query Match 69.1%; Score 860.5; DB 1; Length 234;  
Best Local Similarity 69.6%; Pred. No. 3.3e-78;  
Matches 167; Conservative 28; Mismatches 38; Indels 7; Gaps 2;

Qy 1 MEPGLQAGSCGAPSPDPAMQVQGSVASPWRSTPRWSTSRSYFLSTAL-VCLVAV 59  
Db 1 MDPGLQALNGMAPGPDAMHVPAGSVAS-----HLGTTSRSYFLTTATLALCLVFTV 54  
Qy 60 AILVLVQKDKSTPNTTEKAPLKGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLS 119  
Db 55 ATIMVLVQRTDSIPNSPDNVPKGCNSEDLLCILKRAPPFKSWAYLQVAKHLNNTKLS 114  
Qy 120 WNEDGTIHLIYQDGNLIYVQFPLGLFIYVQQLQFLVQCSNHSVDLTQLLINSKIKKQTLV 179  
Db 115 WNKDGLHGVRYQDGNLIYVQFPLGLFIYVQQLQFLVQCPNNSVDLLELLINKHIKKQALV 174  
Qy 180 TVCESGVQSKNIYQNSQFLHLYLVQVNSTISVRVDFQVDTNTPFLDNVLSVFLYSSSD 239  
Db 175 TVCESGMQTKHYVQNSQFLLDYLVQNTTISVNVDTFQYIDTSTFPLENVLSIFLYSNSD 234

## RESULT 10

US-08-570-923-8  
; Sequence 8, Application US/08570923  
; Patent No. 5677430  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/570,923  
FILING DATE: 12-DEC-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,989  
FILING DATE: 12 APRIL 1994  
APPLICATION NUMBER: US 07/966,775  
FILING DATE: 27-OCT-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992

QY	120	WNEDGTHGLIYVQFPGLYFIVCQLQFLVQCNSHSDLTQLLINSKI       :    :     :     :     :     :     :            :    :     :     :     :     :     :
Db	115	WNKGDLHGVRXQGNLVIQFPGLYFIICQLQFLVQCPNNSVDLKLELLINKHI       :    :     :     :     :     :     :            :    :     :     :     :     :     :
QY	180	TVCESGVOSKNIYNLSOLFLLHYLQVNSTISRVDNFYXDVTNTFPPLDNLVSFFI       :    :     :     :     :     :     :            :    :     :     :     :     :     :
Db	175	TVCESGMOTKHVQNLSOFLLDYLQVNNTISVNDTFQYIDTSTPELVNSIF       :    :     :     :     :     :     :            :    :     :     :     :     :     :
RESULT 12		
US-09-079-785-8		
; Sequence 8, Application US/09079785		
; Patent No. 6143869		
; GENERAL INFORMATION:		
; APPLICANT: Goodwin, Raymond G.		
; APPLICANT: Smith, Craig A.		
; APPLICANT: Armitage, Richard J.		
; APPLICANT: Gruss, Hans-Jürgen		
; TITLE OF INVENTION: NO. 6143869el cytokine That Binds CD30		
; NUMBER OF SEQUENCES: 23		
; CORRESPONDENCE ADDRESS:		
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation		
; STREET: 51 University Street		
; CITY: Seattle		
; STATE: Washington		
; COUNTRY: USA		
; ZIP: 98101		
; COMPUTER READABLE FORM:		



;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: Apple Macintosh  
;; OPERATING SYSTEM: Apple 7.1  
;; SOFTWARE: Microsoft Word, Version 5.1a  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/079,785  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/225,989  
;; FILING DATE: 12 APRIL 1994  
;; APPLICATION NUMBER: US 07/966,775  
;; FILING DATE: 27-OCT-1992  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 907,224  
;; FILING DATE: 01-JUL-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 899,660  
;; FILING DATE: 15-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 892,459  
;; FILING DATE: 02-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 889,717  
;; FILING DATE: 26-MAY-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Seese, Kathryn A.  
;; REGISTRATION NUMBER: 32,172  
;; REFERENCE/DOCKET NUMBER: 2804-E  
;; TELEPHONE: (206)587-0430  
;; TELEFAX: (206)233-0644  
;; TELEX: 756822  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 234 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-09-079-785-8

Query Match 69.1%; Score 860.5; DB 4; Length 234;  
Best Local Similarity 69.6%; Pred. No. 3.3e-78;  
Matches 167; Conservative 28; Mismatches 38; Indels 7; Gaps 2;

Qy 1 MEPGLQQAGSCAPSPDPAMQVQPSVASPWRSTSRYSFYLSLTAL-VCLVAV 59  
Db 1 MDPGLQALNGMAPPGDTAMHVPAGSVAS-----HLGTTSRYSFYLTATLALCLVFTV 54  
Qy 60 AILVLVVKKDDTPTNTTEKAPLKGNCSEDLFCTLKSTPSKKSWAYLOVSKHLNNTKLS 119  
Db 55 ATIMVLVQVORTDSIPNSPNDVPLKGNCSEDLCLIKRAPFKKSWAYLOVAKHLNNTKLS 114  
Qy 120 WNEGTTHGLIYQDGNLIYQFGLFIVQLOFLVQCSNHSVDLTQLLINSKIKKQTLV 179  
Db 115 WNKDGLHGVRYQDGNLIYQFGLFIVQLOFLVQCPNNSVDLKLLELNKHKIKQALV 174  
Qy 180 TVCESGVQSKNIYQNLQFLLHLYQVNSTISVRVDFNVQVYDNTFPLDNVLSVLYSSD 239  
Db 175 TVCESGMOTKHVYQNLQFLLDYLQVNTTISVNVDTFQYIDTSTFPLENVLSIFLYSNSD 234

RESULT 13  
US-08-225-989-23  
; Sequence 23, Application US/08225989  
; Patent No. 5480981  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen

;; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30  
;; NUMBER OF SEQUENCES: 23  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
;; STREET: 51 University Street  
;; CITY: Seattle  
;; STATE: Washington  
;; COUNTRY: USA  
;; ZIP: 98101  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: Apple Macintosh  
;; OPERATING SYSTEM: Apple 7.1  
;; SOFTWARE: Microsoft Word, Version 5.1a  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/225,989  
;; FILING DATE: 12 APRIL 1994  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 907,224  
;; FILING DATE: 01-JUL-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 899,660  
;; FILING DATE: 15-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 892,459  
;; FILING DATE: 02-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 889,717  
;; FILING DATE: 26-MAY-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Seese, Kathryn A.  
;; REGISTRATION NUMBER: 32,172  
;; REFERENCE/DOCKET NUMBER: 2804-E  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206)587-0430  
;; TELEFAX: (206)233-0644  
;; TELEX: 756822  
;; INFORMATION FOR SEQ ID NO: 23:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 215 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-225-989-23

Query Match 65.4%; Score 814.5; DB 1; Length 215;  
Best Local Similarity 70.8%; Pred. No. 1.1e-73;  
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

Qy 20 MQVQPGSVASPWRSTSRYSFYLSLTAL-VCLVAVAILVLVQVKDSTPNTTE 78  
Db 1 MHPVAGSVAS-----HLGTTSRYSFYLTATLALCLVFTVATIMVLVQVORTDSIPNSPD 54  
Qy 79 KAPLKGNCSEDLFCTLKSTPSKKSWAYLOVSKHLNNTKLSWNEBDGTIHLIYQDGNLI 138  
Db 55 NVPLKGNCSEDLCLIKRAPFKKSWAYLOVAKHLNNTKLSWNEBDGTIHLIYQDGNLI 114  
Qy 139 QFGLFIVQLOFLVQCSNHSVDLTQLLINSKIKKQTLVTVCESGVQSKNIYQNLQF 198  
Db 115 QFGLFYIICQLOFLVQCPNNSVDLKLLELNKHKIKQALVTVCESGMOTKHVYQNLQF 174  
Qy 199 LLHYLVQVNSTISVRVDFNVQVYDNTFPLDNVLSVLYSSD 239  
Db 175 LLDYLQVNTTISVNVDTFQYIDTSTFPLENVLSIFLYSNSD 215

RESULT 14

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Qy 139 QPGLYFIVCOLQFLVOCNSHNSVDLTQLLINSKIKKOTLTVTVCESGVQSKNIYQNLSQF 179
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Db 115 QPGLYFIICOLQFLVQCPNNSVDLKLLELLINKHIKKQALVTVCESGMOTKHVYQNLSQF 174
Qy 199 LLHYLVNNTSLSVRDNFQYVDNTFRPLDNVLSVFLYSSSD 239
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 175 LLDYLVNNTSLSVNVDTFQYIDTSTFFPENVLISFLYNSD 215

RESULT 15
US-08-580-014-23
; Sequence 23, Application US/08580014
; Patent No. 5753203
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,014
; FILING DATE: 20-DEC-1995
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELE: 756822
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-580-014-23

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Query Match 65.4%; Score 814.5; DB 1; Length 215;  
Best Local Similarity 70.6%; Pred. NO. 1.1e-73;

**Matches** 156; **Conservative** 26; **Mismatches** 32; **Indels** 7; **Gaps** 2;

Qy	20	MQVOPGSVPWRSRTPWRSRSTSRSYFLSTTAL-VCLVVAVAIILVLLVYOKKDSPTNTTE	78
Db	1	MHPVPGSVAS-----HLGTPSRSSYFLTTATLALCLVFTVATIMVLVYQRTDSIPNSPD	54
Qy	79	KAPLKGNCSEDLFCTLKSTPSPKSSWAYLQVSKHLNNTKLSNEDCTIHGLIYQDGNLIV	138
Db	55	NVPLKGNCSEDLILCKRAPPKSWAYLQVAKHLNNTKLSNKGDKILHGVRVYQDGNLVI	114
Qy	139	QFPGLYFIVCQLQFLVQCSNHSVDLTLOLLINSKIKQTLVTVCSGVQSKNIQNLQSF	198
Db	115	QFPGLYFIICQLQFLVQCPNNSVDLKLLELLINKHKQALVTVCSGMQTKHVYQNLQSF	174
Qy	199	LLHYLQVNSTISVRVNFQVYDNTFPLDNVLSFVLYSSSD	239
Db	175	LLDYLVQNTTISVNDTFYDITSTFPLENLVLSIFLYSNSD	215

Search completed: September 5, 2001, 10:23:10  
Job time: 85 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2001, 10:21:45 ; Search time 44.86 Seconds  
(without alignments)  
322.986 Million cell updates/sec

Title: US-09-628-126-6  
Perfect score: 1246  
Sequence: 1 MEPLQAGSCGAPSPDPAM.....DTNTPPLDNLVSFLYSSD 239

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
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9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
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17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
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20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1246	100.0	239	14 AAR45008	Sequence encoded b
2	1141	91.6	220	14 AAR45006	Sequence encoded b
3	860.5	69.1	234	14 AAR45009	Sequence encoded b
4	814.5	65.4	215	14 AAR45007	Sequence encoded b
5	742	59.6	143	21 AAR08277	Amino acid sequenc
6	600	48.2	143	21 AAR08276	Amino acid sequenc
7	126	10.1	279	17 AAR88357	Mouse Fas ligand.
8	123	9.9	279	16 AAR79098	Mouse Fas ligand.
9	110	8.8	279	16 AAR77282	Mouse Fas-L protei
10	109	8.7	179	16 AAR79069	Mouse Fas ligand (
11	102	8.2	278	16 AAR79095	Rat Fas ligand enc

12	102	8.2	278	20 AAR98069	Rat Fas ligand (Fa
13	102	8.2	278	20 AAR95040	Rat FasL protein.
14	97	7.8	138	16 AAR79068	Mouse Fas ligand (
15	97	7.8	143	21 AAB08266	Amino acid sequenc
16	95.5	7.7	258	20 AAY04371	Human Fas ligand d
17	95	7.6	137	16 AAR79067	Mouse Fas ligand (
18	92	7.4	271	20 AAY28596	Fas ligand (FasL)
19	91	7.3	179	16 AAR79066	Rat Fas ligand (pa
20	91	7.3	309	18 AAR64189	Murine 4-1BB-L pol
21	91	7.3	309	18 AAW26656	Murine 4-1BB ligand
22	89.5	7.2	268	19 AAW48953	Non-cleavable Fas
23	88.5	7.1	448	21 AAB28694	Fc-muAGP-1 (99-291
24	88	7.1	281	20 AAY04373	Human Fas ligand d
25	88	7.1	281	21 AAY87576	Human Fas ligand (
26	88	7.1	281	21 AAY87581	Human Fas ligand (
27	87	7.0	265	19 AAW48954	Non-cleavable Fas
28	87	7.0	277	20 AAY04372	Human Fas ligand d
29	87	7.0	281	16 AAR77281	Human Fas-L protei
30	87	7.0	281	16 AAR79097	Human Fas ligand.
31	87	7.0	281	17 AAR98104	Human Fas ligand d
32	87	7.0	281	17 AAR88356	Human Fas ligand.
33	87	7.0	281	18 AAW27143	Human Fas ligand.
34	87	7.0	281	19 AAW75959	Human Fas ligand.
35	87	7.0	281	19 AAW49105	Fas Ligand. Mamma
36	87	7.0	281	20 AAY28594	Wild type Fas liga
37	87	7.0	281	20 AAW98071	Human Fas ligand (
38	87	7.0	281	20 AAW95041	Human FasL protein
39	87	7.0	281	21 AAB19342	Amino acid sequenc
40	87	7.0	281	21 AAY87569	Human Fas ligand (
41	87	7.0	281	21 AAY87577	Human Fas ligand (
42	87	7.0	281	21 AAY87578	Human Fas ligand (
43	87	7.0	281	21 AAY87579	Human Fas ligand (
44	87	7.0	281	21 AAY87582	Human Fas ligand (
45	87	7.0	2013	21 AAB18265	Plasmodium falcipa

#### ALIGNMENTS

RESULT 1  
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ID AAR45008 standard; Protein; 239 AA.  
XX  
AC AAR45008;  
XX  
DT 19-JUN-1994 (first entry)  
XX  
DE Sequence encoded by a murine CD30-L cDNA clone  
DE encoding additional N-terminal amino acids.  
XX  
KW Hodgkin's disease; lymphoma; surface antigen; cytokine;  
KW CD30 ligand; CD30-L; TNF; NGF.  
XX  
OS Acromys calhirusus.  
XX  
FH Key Location/Qualifiers  
FT Region 47..67  
FT /label- Transmembrane  
XX  
PN WO9324135-A.  
XX  
PD 09-DEC-1993.  
XX  
PF 25-MAY-1993; 93WO-US04926.  
XX  
PR 26-MAY-1992; 92US-0889717.  
PR 02-JUN-1992; 92US-0892459.  
PR 15-JUN-1992; 92US-0899660.  
PR 01-JUL-1992; 92US-0907224.  
PR 27-OCT-1992; 92US-0966775.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX

PI Armitage RJ, Goodwin RG, Smith CA;

XX WPI; 1993-405417/50.

DR N-PSDB; AAQ53537.

XX New cytokine, CD30-L, which binds CD30 - used for developing

PT prods. for diagnosis, detection, purifications, research and

PT therapy

XX Claim 15; Figure 6a; 59pp; English.

XX CD30-L is a ligand for CD30, the 120kd surface antigen widely used

XX as a clinical marker for Hodgkin's lymphoma and related haematologic

XX malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-

XX L and other derived prods. can be used for elucidating the roles

XX that CD30 and CD30-L may play in the immune system and for diagnosis

XX and therapy. It can be isolated as follows. A cDNA library, prep'd from

XX the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion

XX protein labelled with (125)I to obtain cDNA encoding murine CD30-L

XX (AAQ53535). This cDNA can then be used as a probe to screen a human PBL

XX cDNA library to obtain cDNA encoding human CD30-L (AAQ53536). An

XX anchored PCR technique was employed to isolate CD30-L human and murine

XX clones containing an additional 19 N-terminal amino acid sequence

XX (AAQ53537, AAQ53538).

XX SQ Sequence 239 AA;

Query Match 100.0%; Score 1246; DB 14; Length 239;

Best Local Similarity 100.0%; Pred. No. 1.4e-116;

Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGPLQAGSGCAPSPDPAMQVPGSVASGSPWRSTRPWRSTRSYFYLTALVCLVAVVA 60

DB 1 mepglqagsgcagcpdpamqvpqsvasgspwrstrpwrstrsyfystaltclvavva 60

QY 61 IILVLVQKKSTPNTEKAPLKGNCSEDLFCTLKSTPKSKSWAYLQVSKHLNNTKLSW 120

DB 61 iilvlvqkkdstpnttekaplkgncsedlftclstpskkswaylqvskhlntklsw 120

QY 121 NEDGTIHLGLIYQDGNLIVQFPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLVT 180

DB 121 nedgtihlgllyqdgngllyqfpglyfivcqlqflvqcsnhsvdltqlllnskikkqtlvt 180

QY 181 VCESGVQSKNIYQNLISQFLLHVLQVNSTISVRVDNFQYVDTNFTPLDNVLSVFLYSSSD 239

DB 181 vcesgvqskniyqnlisqfllhylvqnstisvrvdnfyvdtntfpldnvlsvflysssd 239

RESULT 2

AAR45006

ID AAR45006 standard; Protein; 220 AA.

XX AAR45006;

XX 19-JUN-1994 (first entry)

XX Sequence encoded by a murine CD30-L cDNA clone.

XX Hodgkin's disease; lymphoma; surface antigen; cytokine;

KW CD30 ligand; CD30-L; TNF; NGF.

XX Acomys cahirinus.

XX Key Location/Qualifiers

FT Region 28..48

FT /label= transmembrane

XX WO9324135-A.

XX 09-DEC-1993.

XX 25-MAY-1993; 93WO-US04926.

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XX 26-MAY-1992; 92US-0889717.

PR 02-JUN-1992; 92US-0892459.

PR 15-JUN-1992; 92US-0899660.

PR 01-JUL-1992; 92US-0907224.

PR 27-OCT-1992; 92US-0966775.

XX (IMMV ) IMMUNEX CORP.

XX Armitage RJ, Goodwin RG, Smith CA;

XX WPI; 1993-405417/50.

DR N-PSDB; AAQ53535.

XX New cytokine, CD30-L, which binds CD30 - used for developing

PT prods. for diagnosis, detection, purifications, research and

PT therapy

XX Claim 15; Figure 3a; 59pp; English.

XX CD30-L is a ligand for CD30, the 120kd surface antigen widely used

XX as a clinical marker for Hodgkin's lymphoma and related haematologic

XX malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-

XX L and other derived prods. can be used for elucidating the roles

XX that CD30 and CD30-L may play in the immune system and for diagnosis

XX and therapy. It can be isolated as follows. A cDNA library, prep'd from

XX the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion

XX protein labelled with (125)I to obtain cDNA encoding murine CD30-L

XX (AAQ53535). This cDNA can then be used as a probe to screen a human PBL

XX cDNA library to obtain cDNA encoding human CD30-L (AAQ53536). An

XX anchored PCR technique was employed to isolate CD30-L human and murine

XX clones containing an additional 19 N-terminal amino acid sequence

XX (AAQ53537, AAQ53538).

XX SQ Sequence 220 AA;

Query Match 91.6%; Score 1141; DB 14; Length 220;

Best Local Similarity 100.0%; Pred. No. 3.9e-106;

Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 MQVOPGVSASVPWRSTRPWRSTRSYFYLTALVCLVAVVAIILVYVQKKDSTPTTTEK 79

DB 1 mqvopgvsasvpwrstrpwrstrsyfystaltclvavavaiilvvvqkkdstptttek 60

QY 80 APLKGGNCSEDLFCTLKSTPKSKSWAYLQVSKHLNNTKLSWNEGTIHLGLIYQDGNLIVQ 139

DB 61 aplkggncsedlftclstpskkswaylqvskhlntklswnedgtihlgllyqdgngllyq 120

QY 140 FPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLVTVCSGVQSKNIYQNLISQFL 199

DB 121 fpglyfivcqlqflvqcsnhsvdltqlllnskikkqtlvtvcsesgvqskniyqnlisqfl 180

QY 200 LHYLVQVNSTISVRVDNFQYVDTNFTPLDNVLSVFLYSSSD 239

DB 181 lhylvqnstisvrvdnfyvdtntfpldnvlsvflysssd 220

RESULT 3

AAR45009

ID AAR45009 standard; Protein; 234 AA.

XX AAR45009;

XX 19-JUN-1994 (first entry)

XX Sequence encoded by a human CD30-L cDNA clone

DE encoding additional N-terminal amino acids.

XX Hodgkin's disease; lymphoma; surface antigen; cytokine;

KW CD30 ligand; CD30-L; TNF; NGF.

XX Homo sapiens.

OS Key Location/Qualifiers

FT Region 41..62

FT XX /label= Transmembrane

PN W09324135-A.

PD 09-DEC-1993.

XX 25-MAY-1993; 93WO-US04926.

XX 26-MAY-1992; 92US-0889717.

PR 02-JUN-1992; 92US-0892459.

PR 15-JUN-1992; 92US-0899660.

PR 01-JUL-1992; 92US-0907224.

PR 27-OCT-1992; 92US-0966775.

XX (IMMV ) IMMUNEX CORP.

PI Armitage RJ, Goodwin RG, Smith CA;

DR WPI; 1993-405417/50.

DR N-PSDB; AAQ53538.

XX New cytokine, CD30-L, which binds CD30 - used for developing

PT prods. for diagnosis, detection, purifications, research and

PT therapy

XX Claim 15; Figure 7a; 59pp; English.

XX CD30-L is a ligand for CD30, the 120kd surface antigen widely used

CC as a clinical marker for Hodgkin's lymphoma and related haematologic

CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-

CC L and other derived prods. can be used for elucidating the roles

CC that CD30 and CD30-L may play in the immune system and for diagnosis

CC and therapy. It can be isolated as follows. A cDNA library prepd. from

CC the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion

CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L

CC (AAQ53535). This cDNA can then be used as a probe to screen a human PBL

CC cDNA library to obtain cDNA encoding human CD30-L (AAQ53536). An

CC anchored PCR technique was employed to isolate CD30-L human and murine

CC clones containing an additional 19 N-terminal amino acid sequence

CC (AAQ53537, AAQ53538).

XX Sequence 234 AA;

Query Match 69.1%; Score 860.5; DB 14; Length 234;

Best Local Similarity 69.6%; Pred. No. 4.6e-78;

Matches 167; Conservative 28; Mismatches 38; Indels 7; Gaps

2;

Qy 1 MBPGLQAGSCGAPDPDPAMQVPGSVASWPRSRPWRSTSRFYSLSTTAL-VCLVAV 59

Db 1 mdpglqalngmappgdmtamhvpagsvas-----hlggttsrsyfytatlalclvftv 54

Qy 60 AITLVLVOKDSTPNTTEKAPLKGNCSEDLCTLKSTPSKSWAYLOVSKHLNNTKLS 119

Db 55 atlmvlvrtidsipnsdpnvpkgncsedllcailkrpfkkswaylqvakhnkckls 114

Qy 120 WNEDEPTIHLITQDGNLIYQFPGLYFIVCOLQFLVQCSNHSVDLTQLLNSKIKKQTLV 179

Db 115 wnkdgilhvrydgnlvlfpglyfiicqlqlvqcpnnsvdiklellnkhhkqalv 174

Qy 180 TVCESGVQSKNIYONISQELLLHYLQVNSTISVRVDFNFQYVDNTFPDLNLSVFLYSSD 239

Db 175 tvcesgmqtkhvygnlsqfildylqvnvtissvndtftqyidstfplenvlsiflynsd 234

RESULT 4

AAR45007

ID AAR45007 standard; Protein; 215 AA.

XX AC AAR45007;

XX DT 19-JUN-1994 (first entry)

XX

DE XX Sequence encoded by a human CD30-L cDNA clone.

KW Hodgkin's disease; lymphoma; surface antigen; cytokine;

KW CD30 ligand; CD30-L; TNF; NGF.

OS Homo sapiens.

EH Key Location/Qualifiers

FT Region 22..43

FT /label= transmembrane

PN W09324135-A.

XX 09-DEC-1993.

XX 25-MAY-1993; 93WO-US04926.

XX 26-MAY-1992; 92US-0889717.

XX 02-JUN-1992; 92US-0892459.

XX 15-JUN-1992; 92US-0899660.

XX 01-JUL-1992; 92US-0907224.

XX 27-OCT-1992; 92US-0966775.

XX (IMMV ) IMMUNEX CORP.

XX Armitage RJ, Goodwin RG, Smith CA;

XX WPI; 1993-405417/50.

XX N-PSDB; AAQ53536.

XX New cytokine, CD30-L, which binds CD30 - used for developing

PT prods. for diagnosis, detection, purifications, research and

PT therapy

XX Claim 15; Figure 5a; 59pp; English.

XX CD30-L is a ligand for CD30, the 120kd surface antigen widely used

CC as a clinical marker for Hodgkin's lymphoma and related haematologic

CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-

CC L and other derived prods. can be used for elucidating the roles

CC that CD30 and CD30-L may play in the immune system and for diagnosis

CC and therapy. It can be isolated as follows. A cDNA library prepd. from

CC the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion

CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L.

CC This cDNA can then be used as a probe to screen a human PBL cDNA

CC library to obtain cDNA encoding human CD30-L.

XX Sequence 215 AA;

Query Match 65.4%; Score 814.5; DB 14; Length 215;

Best Local Similarity 70.6%; Pred. No. 1.6e-73;

Matches 156; Conservative 26; Mismatches 33; Indels 7; Gaps

2;

Qy 20 MOVPGSVASWPRSRPWRSTSRFYSLSTTAL-VCLVAVAILLVVQKDKSTPNTTE 78

Db 1 mhvpagsvas-----hlggttsrsyfytatlalclvftvatimlvvqrdtsipnsd 54

Qy 79 KAPLKGNCSEDLCTLKSTPSKSWAYLOVSKHLNNTKLSWNEDEPTIHLITQDGNLIV 138

Db 55 nvplkpgncsedllcailkrpfkkswaylqvakhnkcklswnkdgilhvryqdgnlvi 114

Qy 139 QPFGLYFIVCOLQFLVQCSNHSVDLTQLLINSKIKKQTLVTVCSGVQSKNIYONLSQF 198

Db 115 qfpglyfiicqlqlvqcpnnsvdiklellnkhhkqalvtvcesgmqtkhvygnlsqf 174

Qy 199 LLHYLQVNSTISVRVDFNFQYVDNTFPDLNLSVFLYSSD 239

Db 175 lldylqvnvtissvndtftqyidstfplenvlsiflynsd 215

RESULT 5

AAB08277

ID	AA08277	standard; Protein; 143 AA.
XX	XX	
AC	AA08277;	
XX	XX	
DT	04-DEC-2000	(first entry)
XX	XX	
DE	Amino acid sequence of a mouse TNF ligand CD30L.	
XX	XX	
KW	AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;	
KW	type II transmembrane protein; B cell stimulatory factor;	
KW	inflammatory disorder; immune disorder; rheumatoid arthritis;	
KW	lupus and graft versus host disease.	
XX	XX	
OS	Mus sp.	
XX	XX	
PN	W0200047740-A2.	
XX	XX	
PD	17-AUG-2000.	
XX	XX	
PF	11-FEB-2000; 2000WO-US03653.	
XX	XX	
PR	12-FEB-1999; 99US-0119906.	
PR	18-NOV-1999; 99US-0166271.	
XX	XX	
PA	(AMGE-) AMGEN INC.	
XX	XX	
PI	Boyle WJ, Hsu H;	
XX	XX	
DR	WPI; 2000-558217/51.	
XX	XX	
PT	Novel polypeptides comprising tumour necrosis factor ligand family	
PT	proteins, useful for treating inflammatory and immune disorders, e.g.	
PT	rheumatoid arthritis -	
XX	XX	
PS	Claim 14; Fig 9; 71pp; English.	
XX	XX	
CC	AA08265-83 represent tumour necrosis factor (TNF) ligands. The	
CC	specification describes an AGP-3 polypeptide, which is TNF ligand	
CC	family member. AGP-3 is a type II transmembrane protein, and is a	
CC	potent B cell stimulatory factor. Expression of AGP-3 correlates to	
CC	increases in the number of B cells and immunoglobulins produced.	
CC	AGP-3 proteins, antibodies, and nucleic acids may be used to treat	
CC	inflammatory and immune disorders, e.g. rheumatoid arthritis,	
CC	Crohn's disease, lupus and graft versus host disease. The nucleic	
CC	acids may be used to regulate the expression of an AGP-3 related	
CC	protein. The AGP-3 proteins, antibodies and nucleic acids are also	
CC	useful for the detection of AGP-3 agonists, antagonists and	
CC	characterizing interactions with AGP-3 related proteins.	
XX	XX	
SQ	Sequence 143 AA;	
	Query Match 59.6%; Score 742; DB 21; Length 143;	
	Best Local Similarity 100.0%; Pred. No. 1.6e-66;	
	Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps	
QY	97 STPSKSWAYLQVSKHLNNTKLSWNEDGTIHGIYODGNLIYFPGLYFIVCOQLFVOC	156
	1 stpskswaylqvsckhlntklswnedgtihgiyodgnliyfpglyfivcoqlfivqc	160
Db	1 stpskswaylqvsckhlntklswnedgtihgiyodgnliyfpglyfivcoqlfivqc	160
QY	157 SNHSVDLTQLLNSKIKKOTLVTVCESGVQSKNIYONLSQFLLHYLVQNSTISVRDNF	216
	1 snhsvdltqllnskikkqlvtvcesgvqskniyqnlsgfllhylvqnstisvrndf	220
Db	61 snhsvdltqllnskikkqlvtvcesgvqskniyqnlsgfllhylvqnstisvrndf	120
QY	217 QYVDNTFPDLNLSVFLYSSSD 239	
	1 qyvdntfpdlndvlsflysssd	243
Db	121 qyvdntfpdlndvlsflysssd 143	
RESULT	6	
AA08276		
ID	AA08276	standard; Protein; 143 AA.
XX	XX	

AC	AA808276;	
XX		
DT	04-DEC-2000 (first entry)	
XX		
DE	Amino acid sequence of a human TNF ligand CD30L.	
XX		
KW	AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;	
KW	type II transmembrane protein; B cell stimulatory factor;	
KW	inflammatory disorder; immune disorder; rheumatoid arthritis;	
KW	lupus and graft versus host disease.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200047740-A2.	
XX		
PD	17-AUG-2000.	
XX		
PF	11-FEB-2000; 2000WO-US03653.	
XX		
PR	12-FEB-1999; 99US-0119906.	
PR	18-NOV-1999; 99US-0166271.	
XX		
PA	(AMGE-) AMGEN INC.	
XX		
PI	Boyle WJ, Hsu H;	
XX		
DR	WPI; 2000-558217/51.	
XX		
PT	Novel polypeptides comprising tumour necrosis factor ligand family	
PT	proteins, useful for treating inflammatory and immune disorders, e.g.	
PT	rheumatoid arthritis -	
XX		
PS	Claim 14; Fig 9; 71pp; English.	
XX		
CC	AA808265-83 represent tumour necrosis factor (TNF) ligands. The	
CC	specification describes an AGP-3 polypeptide, which is TNF ligand	
CC	family member. AGP-3 is a type II transmembrane protein, and is a	
CC	potent B cell stimulatory factor. Expression of AGP-3 correlates to	
CC	increases in the number of B cells and immunoglobulins produced.	
CC	AGP-3 proteins, antibodies, and nucleic acids may be used to treat	
CC	inflammatory and immune disorders, e.g. rheumatoid arthritis,	
CC	Crohn's disease, lupus and graft versus host disease. The nucleic	
CC	acids may be used to regulate the expression of an AGP-3 related	
CC	protein. The AGP-3 proteins, antibodies and nucleic acids are also	
CC	useful for the detection of AGP-3 agonists, antagonists and	
CC	characterizing interactions with AGP-3 related proteins.	
XX		
SQ	Sequence 143 AA;	
	Query Match 48.2%; Score 600; DB 21; Length 143;	
	Best Local Similarity 77.3%; Pred. No. 2.6e-52;	
	Matches 109; Conservative 19; Mismatches 13; Indels 0; Gaps	
QY	99 PSKSWAYLQVSKHLNNTKLSWNGDTIHLIVODGNLIVQFGLYFVCGLOFLVQCSN 158	
	1	
Db	3 pfkkswaylvqakhlntklswnkdglhlhrryqdgnglvqfpglyflicqlgflvqcpn 62	
	1	
QY	159 HSDVLTQLLINSKIKQTLTVTCESGVQSKNIYQNLISQFLHLHYLQVNSTISVRVDNFQY 218	
	:	
Db	63 nsvdklelllnkhikqalvtvcesgmqtqkhyqnlsgfildylqvmttisvndvtfqy 122	
QY	219 VDTWTFPLDNLVSFLYSSSD 239	
	:	
Db	123 idtftfplenvlsiflysnsd 143	
RESULT	7	
AA888357		
ID	AA888357 standard; Protein; 279, AA.	
XX		
AA888357;		
XX		

AC	AAK79098;	
XX	21-FEB-1996 (first entry)	
XX	Mouse Fas ligand.	
XX	Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;	
KW	Fas cell surface antigen; Fas-L; mouse.	
XX	Mus musculus.	
OS		
XX		
XX		
PH	Location/Qualifiers	
FT	25..78	
Region	/label= proline-rich	
FT	79..100	
Domain	/label= transmembrane_anchor	
FT	/note= "hydrophobic"	
FT	117	
Modified-site	/label= N-glycosylation_site	
FT	131	
Modified-site	/label= N-glycosylation_site	
FT	182	
Modified-site	/label= N-glycosylation_site	
FT	248	
Modified-site	/label= N-glycosylation_site	
FT	258	
Modified-site	/label= N-glycosylation_site	
XX		
XX	WO9513293-A1.	
PN		
XX	18-MAY-1995.	
PD		
XX	10-NOV-1994; 94WO-JP01899.	
XX	18-OCT-1994; 94JP-0278378.	
PR	10-NOV-1993; 93JP-0305975.	
PR	13-DEC-1993; 93JP-0342526.	
PR	18-MAR-1994; 94JP-0074344.	
PR	08-JUL-1994; 94JP-0180955.	
PR	07-SEP-1994; 94JP-0239363.	
XX		
PA	(MOCH ) MOCHIDA PHARM CO LTD.	
PA	(OSAB-) OSAKA BIOSCIENCE INST.	
XX	Nagata S, Nakamura N, Suda T, Takahashi T;	
PI		
XX	WPI; 1995-194031/25.	
DR	N-PSDB; AAQ94156, AAQ99499.	
XX		
PT	Peptide which binds to Fas antigen, and antibody reactive with it	
PT	for treatment and diagnosis of viral or auto-immune diseases	
XX		
PS	Claim 12; Fig 23-24; 300pp; Japanese.	
XX		
CC	A clone (AAQ94156) contg. an insert coding for the mouse Fas ligand	
CC	was isolated using probes derived from a rat Fas-L clone (see	
CC	AAQ94153). The mouse sequence contains an open reading frame coding	
CC	for a 279 amino acid sequence with 5 N-glycosylation sites and a	
CC	proline-rich region. The deduced mouse amino acid sequence has	
CC	91.4% homology with rat Fas-L. Fas ligands are able to induce	
CC	apoptosis in cells which express the Fas cell surface antigen.	
XX		
SQ	Sequence 279 AA;	
	Query Match 9.9%; Score 123; DB 16; Length 279;	
	Best Local Similarity 22.5%; Pred. No. 0.0003;	
	Matches 55; Conservative 43; Mismatches 96; Indels 50; Gaps	
Qy	10 SCG-----ASPDPAHQVQCSVAPRSTPWRSTSR-----YFYLSTTALV 53	
Db	34 scgrrgdrpppppppslpbpsqglppltplkkkdhntnlwlpvffmvlvalv 93	



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QY 54 CLWVAAILVLVQKDDSTPNTTEKAPLKGGNCSEDLFCTLKSTPSKK-----SWAYLQV 109
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
94 gm-glgmvgqlfhqlkelaelftnqslkvssfekqi--anpstpskkeprsvahlgt 149
QY 110 SKHLNNTKLSWNED-GT--IHGLIYODGNLIYQFPGLYFIVCOLOFLVQ-CSNHSVDLT 165
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
150 nphrsiplededygtaligsvkykkgglvinetgylfyskvyfrgscnqplnhkv 209
QY 166 QLLINSK-----IKQTLLVTVCESG-----VOSKNYQNLQFLFLHYLQ 204
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
210 ymr-nskypedivlmeekrlnycttqgiwahssylgavfnlttsadhllyvnisqlsinfe 268
QY 205 VNST 208
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
269 eskt 272

RESULT 9
AAR77282
ID AAR77282 standard; Protein; 279 AA.
XX AC AAR77282;
XX DT 05-DEC-1995 (first entry)
XX DE Mouse Fas-L protein.
XX KW Fas ligand; Fas-L; cell surface protein; autoimmune disease;
XX KW self-tolerance.
XX OS Mus sp.
XX FH Key Location/Qualifiers
XX FT Domain 1..78
XX FT /label= Cytoplasmic_domain
XX FT 79..103
XX FT /label= Transmembrane_domain
XX FT 104..279
XX FT /label= Extracellular_domain
XX PN WO9518819-A.
XX PD 13-JUL-1995.
XX PF 06-JAN-1995; 95WO-US00362.
XX PR 01-FEB-1994; 94US-0190559.
XX PR 07-JAN-1994; 94US-0179138.
XX PA (IMMV ) IMMUNEX CORP.
XX PI Goodwin RG;
XX DR WPI; 1995-255032/33.
XX DR N-PSDB; AAQ91312.
XX PT Human and murine DNA encoding ligand(s) binding to cell surface protein
XX PT Fas - useful for studying auto-immune disorder(s) and development of
XX PT self-tolerance.
XX PS Disclosure; Page 29-30; 38pp; English.
XX CC A cDNA library prep. from mouse peripheral blood lymphocyte mRNA was
XX CC screened with a murine Fas-L probe from the 3' end of Fas-L DNA.
XX CC An isolated clone (AAQ91312) encoded mouse Fas-L.
XX SQ Sequence 279 AA;

```

Query Match 8.8%; Score 110; DB 16; Length 279;  
 Best Local Similarity 21.9%; Pred. No. 0.006;  
 Matches 55; Conservative 42; Mismatches 104; Indels 50; Gaps 11;

```

QY 10 SCG-----ARSPDPAMQVQPSVASPWRSTRPWRSTSRSYFLSTTALVCLWAVA 60
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
34 scgrpgdqrrpppppppsplppspqplpisltpklkkkdh-----tnlwpv 84
QY 61 IILVL-----VQKDDSTPNTTEKAPLKGGNCSEDLFCTLKSTPSKK----- 102
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
85 ffwlqkelaelftnqslqkelaelftnqslkvssfekqi--anpstpskkepr 142
QY 103 SWAYLQVSKHLNNTKLSWNED-GT--IHGLIYODGNLIYQFPGLYFIVCOLOFLVQ-CSN 158
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
143 svahltgnphrsiplededygtaligsvkykkgglvinetgylfyskvyfrgscn 202
QY 159 HSDVLTQLQLINSKIKQTLLVTVCESGVOSKNI-YONLSQFLHLYQNLNSTISVRDNFQ 217
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
203 qplnhkvymr-nskypedivl-----meekrlnyfttqgiwahssylgavfnlttsadhl 255
QY 218 YVDNTNTPFLDN 228
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
256 yvnisqlsin 266

RESULT 10
AAR79069
ID AAR79069 standard; Protein; 179 AA.
XX AC AAR79069;
XX DT 22-FEB-1996 (first entry)
XX DE Mouse Fas ligand (partial sequence).
XX KW Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;
XX KW Fas cell surface antigen; Fas-L; mouse.
XX OS Mus musculus.
XX PN WO9513293-A1.
XX PD 18-MAY-1995.
XX PF 10-NOV-1994; 94WO-JP01899.
XX PR 18-OCT-1994; 94JP-0278378.
XX PR 10-NOV-1993; 93JP-0305975.
XX PR 13-DEC-1993; 93JP-0342526.
XX PR 18-MAR-1994; 94JP-0074344.
XX PR 08-JUL-1994; 94JP-0180955.
XX PR 07-SEP-1994; 94JP-0239363.
XX PA (MOCH ) MOCHIDA PHARM CO LTD.
XX PA (OSAB-) OSAKA BIOSCIENCE INST.
XX PI Nagata S, Nakamura N, Suda T, Takahashi T;
XX DR WPI; 1995-194031/25.
XX DR N-PSDB; AAQ99498.
XX PT Peptide which binds to Fas antigen, and antibody reactive with it
XX PT for treatment and diagnosis of viral or auto-immune diseases
XX PS Claim 11; Page 222-224; 300pp; Japanese.
XX CC Fas ligands or active fragments able to induce apoptosis in cells
XX CC which express the Fas cell surface antigen are claimed. The
XX CC proteins are isolated from human, rat and mouse sources. The present
XX CC sequence represents part of the mouse Fas ligand.
XX SQ Sequence 179 AA;

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Query Match 8.7%; Score 109; DB 16; Length 179;  
 Best Local Similarity 26.2%; Pred. No. 0.0041;  
 Matches 37; Conservative 28; Mismatches 46; Indels 30; Gaps 7;

CC	the protein is a claimed Fas ligand able to induce apoptosis in	
XX	cells which express the Fas cell surface antigen.	
SQ	Sequence	278 AA;
	Query Match	8.2%; Score 102; DB 16; Length 278;
	Best Local Similarity	21.7%; Pred. No. 0.038;
	Matches 52; Conservative	37; Mismatches 105; Indels 46; Gaps 9;
QY	14	PSDPAMQVOPGVSVPWRSTRPWRSTRSYFYLLSTTALVCLVAVAILL---VLVVOK 69
DB	47	ppppppspipppspqppplpplsplkkkdnlelwpivffmivvalvgmgymygfihlqk 106
QY	70	KDSPNTTEKAPLKGGNCSEDLFCTLKSTPSK-----KSWAYLQVSKHNLNNTKLSWNED-G 124
DB	107	elaelreftnshlrvsfekqi--anpstsetkkprsvahltgnprsrslplewedyg 164
QY	125	T--IHGLIYDGNLIIVPGGLYFIVCGLQLVQCQN-----HSV-----DLTLQLL 168
DB	165	talisgvykkggvlvneaglyfyyskvyfrgscnsgplshkvmrnfkyppgdvlvm-- 222
QY	169	INSKIKQTGLVTVCESGVQSKNIYQNLISQFLHLVLYQVNSTISVRVDNFQVVDNTTFPLDN 228
DB	223	-----eeeklynycttg-----qiwahssy'gavfnltvadhllyvnisqlslin 265
	RESULT 12	
	AAW98069	
ID	AAW98069	standard; Protein; 278 AA.
XX	AAW98069;	
XX	21-JUN-1999	(first entry)
XX	Rat Fas ligand (FasL).	
KW	FasL; Fas ligand; proinflammatory; immunosuppressive; rat;	
KW	graft versus host disease; autoimmune disease; psoriasis;	
KW	rheumatoid arthritis; systemic lupus erythematosus; gene therapy.	
OS	Rattus sp.	
XX	Key	Location/Qualifiers
FT	Domain	78..99
FT	/note=	"transmembrane domain"
FT	Modified-site	116
FT	/note=	"N-glycosylated"
FT	Modified-site	130
FT	/note=	"N-glycosylated"
FT	Modified-site	247
FT	/note=	"N-glycosylated"
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XX	WO9903999-A1.	
XX	28-JAN-1999.	
XX	16-JUL-1998;	98WO-US14771.
XX	17-JUL-1997;	97US-0052829.
XX	(UNMI ) UNIV MICHIGAN.	
XX	Chen J, Nabel GJ;	
XX	WPI; 1999-132243/11.	
XX	N-PSDB; AAX24877.	
XX	Inhibition of proinflammatory responses - using an agent which	
PT	modulates FasL stimulation, used for treating graft versus host	
PT	disease or autoimmune disease	

XX PS Disclosure; Fig 4A; 71pp; English.  
 CC This present sequence is rat Fas ligand (FasL). The invention  
 CC provides a method for inhibiting a proinflammatory response in a  
 CC cell mixture by administering an immunosuppressive agent which  
 CC inhibits the proinflammatory activity of FasL. In some embodiments,  
 CC FasL is coadministered with the immunosuppressive agent, and the  
 CC cell mixture comprises neutrophil cells. The method can be  
 CC practised in vitro, ex vivo or in vivo. Suitable immunosuppressive  
 CC agents include antisenescence molecules that inhibit endogenous FasL  
 CC expression, soluble Fas receptors or variants, ribozymes that  
 CC inhibit the endogenous expression of FasL, drugs that inhibit FasL  
 CC signalling, agents that induce the endogenous expression of  
 CC transforming growth factor (TGF)-beta, and polynucleotides coding  
 CC for an immunosuppressive agent such as TGF-beta. The method can be  
 CC used for treating diseases associated with an undesired FasL-mediated  
 CC proinflammatory response, e.g. graft versus host disease, or an  
 CC autoimmune disease such as systemic lupus erythematosus, rheumatoid  
 CC arthritis and psoriasis. The invention also provides a method for  
 CC identifying agents which modulate FasL stimulation of a  
 CC proinflammatory response.  
 XX SQ Sequence 278 AA;

Query Match 8.2%; Score 102; DB 20; Length 278;  
 Best Local Similarity 21.7%; Pred. No. 0.038;  
 Matches 52; Conservative 37; Mismatches 105; Indels 46; Gaps 9;  
 QY 14 PSPDPAMQVQPGSVASPRSTRPWRSTRSRFYFSTLTALVCLVAVAILL----VLVVQK 69  
 Db 47 pppppspplpppsppplpplspkdkndielwlpviffmvlvalvgmglmyqlhqlk 106  
 QY 70 KDSPTNTEKAPLKGNCSEDLFCTLKSTPSK----KSWAYLQVSKHLNNTKLSWNED-G 124  
 Db 107 elaelrefthslrvssfekqi--anpstsetkprsvahltnprsrslplewedyg 164  
 QY 125 T--IHGLIYQDGNLIVOPPGLYFIVCQLFVQCSN-----HSV-----DLTLQLL 168  
 Db 165 talisgvykkgglvineaglyfvyksyfrgqscnspkshkymrnfkypgdvlm-- 222  
 QY 169 INSKIKKQTLVTVCESGVQSKNIYQNLSQLFLHYLQVNSTISVRVDNFQYVDNTFPPLDN 228  
 Db 223 -----eeklnycttg-----qiwahssylgavfultvadhlyvnisqlslin 265

RESULT 13  
 AAW95040  
 ID AAW95040 standard; Protein; 278 AA.  
 XX AC AAW95040;  
 XX DT 14-MAY-1999 (first entry)  
 XX DE Rat FasL protein.  
 XX KW Cell proliferation; FasL protein; pathogen; modulation; cell locus;  
 XX KW proinflammatory response; inhibition; rat.  
 XX OS Rattus sp.  
 XX PN WO9903998-A1.  
 XX PD 28-JAN-1999.  
 XX PF 16-JUL-1998; 98WO-US14770.  
 XX PX 17-JUL-1997; 97US-0052829.  
 XX PA (UNMI ) UNIV MICHIGAN.  
 XX PI Nabel GJ;

XX WPI; 1999-132242/11.  
 DR N-PSDB; AAX21573.  
 XX PT Method for inhibiting proliferation of a cell - comprises  
 XX administration of FasL protein to the cell locus  
 XX PS Disclosure; Fig 6A-C; 70pp; English.  
 XX CC The invention relates to a method for inhibiting the proliferation of a  
 CC suitable cell or pathogen which comprises administering to the cells  
 CC locus an effective amount of FasL. A method for identifying agents which  
 CC modulate FasL stimulation of a localised proinflammatory response is also  
 CC provided. The methods can be used for provoking a proinflammatory  
 CC response in the locus of a cell. It can also be used to inhibit the  
 CC proliferation of a cell or a pathogen in a subject. The present sequence  
 CC represents a rat FasL protein.  
 XX SQ Sequence 278 AA;

Query Match 8.2%; Score 102; DB 20; Length 278;  
 Best Local Similarity 21.7%; Pred. No. 0.038;  
 Matches 52; Conservative 37; Mismatches 105; Indels 46; Gaps 9;  
 QY 14 PSPDPAMQVQPGSVASPRSTRPWRSTRSRFYFSTLTALVCLVAVAILL----VLVVQK 69  
 Db 47 pppppspplpppsppplpplspkdkndielwlpviffmvlvalvgmglmyqlhqlk 106  
 QY 70 KDSPTNTEKAPLKGNCSEDLFCTLKSTPSK----KSWAYLQVSKHLNNTKLSWNED-G 124  
 Db 107 elaelrefthslrvssfekqi--anpstsetkprsvahltnprsrslplewedyg 164  
 QY 125 T--IHGLIYQDGNLIVOPPGLYFIVCQLFVQCSN-----HSV-----DLTLQLL 168  
 Db 165 talisgvykkgglvineaglyfvyksyfrgqscnspkshkymrnfkypgdvlm-- 222  
 QY 169 INSKIKKQTLVTVCESGVQSKNIYQNLSQLFLHYLQVNSTISVRVDNFQYVDNTFPPLDN 228  
 Db 223 -----eeklnycttg-----qiwahssylgavfultvadhlyvnisqlslin 265

RESULT 14  
 AAR79068  
 ID AAR79068 standard; Protein; 138 AA.  
 XX AC AAR79068;  
 XX DT 22-FEB-1996 (first entry)  
 XX DE Mouse Fas ligand (partial sequence).  
 XX KW Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;  
 XX KW Fas cell surface antigen; Fas-L; mouse.  
 XX OS Mus musculus.  
 XX PN WO9513293-A1.  
 XX PD 18-MAY-1995.  
 XX PF 10-NOV-1994; 94WO-JP01899.  
 XX PR 18-OCT-1994; 94JP-0278378.  
 XX PR 10-NOV-1993; 93JP-0305975.  
 XX PR 13-DEC-1993; 93JP-0342526.  
 XX PR 18-MAR-1994; 94JP-0074344.  
 XX PR 08-JUL-1994; 94JP-0180955.  
 XX PR 07-SEP-1994; 94JP-0239363.  
 XX PA (MOCH ) MOCHIDA PHARM CO LTD.  
 XX PA (OSAB-) OSAKA BIOSCIENCE INST.



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OM nucleic - nucleic search, using sw model

Run on: September 5, 2001, 21:46:06 ; Search time 1370.5 Seconds  
(without alignments)  
4572.960 Million cell updates/sec

Title: US-09-628-126-18  
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Searched: 10228115 seqs, 4726426750 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	371.6	56.0	487	170	BF890112	BF890112 289772 MA
5	194.8	29.4	318	144	BF082784	BF082784 PM1-BT075
6	193.8	29.1	463	173	BG091233	BG091233 mac41f02.
7	184.2	27.8	276	118	AW602310	AW602310 RC5-BT055
8	171.6	25.9	277	163	BE073509	BE073509 RC5-BT055
9	131.8	19.9	550	119	AW654920	AW654920 105425 MA
10	122	18.4	552	248	AZ711040	AZ711040 RPCI-24-1
11	56.4	8.5	219	190	W21054	W21054 zb53e12.r1
12	56.4	8.5	524	24	A1734260	A1734260 zb53e12.y
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ALIGNMENTS

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 REFERENCE 1 (bases 1 to 910)  
 AUTHORS Li W.B., Gruber C., Jessee J. and Polayes D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

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 /note="vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 244 a 232 c 204 g 225 t 5 others  
 ORIGIN

Query Match 60.7%; Score 402.6; DB 106; Length 910;  
 Best Local Similarity 78.7%; Pred. No. 3.3e-112;  
 Matches 490; Conservative 3; Mismatches 127; Indels 3; Gaps 1;

Qy 44 CGAGCCCTGGAGAGCACAAGTCCAGCTACTTCTACCTCAGCACCACCGACATGG---100  
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 Qy 101 TGTGCTTTGTGTGTCAGTGGGATCTTCTGCTAGTCCAGAGAAAGAGACTCCA 160  
 Db 330 TGTGCTTTGTGTGTCAGTGGGATCTTCTGCTAGTCCAGAGAAAGAGACTCCA 389  
 Qy 161 CTCCAAATACAACTGAGAGAGGCCCCCTTAAAGAGAGAAATGCTCAGAGAGATCTTCT 220  
 Db 390 TTCCCAACTCAGCTGACAAAGTCCCTCCCTCAAGAGAGAAATGCTCAGAGAGATCTTAT 449  
 Qy 221 GTACCTGAAAGTACTTCAATCCAGAGAGTATGCGGCTTACCTCCAGTGTCAAGCATC 280  
 Db 450 GTATCTGAAAGAGTCCATTCAAAGTATGCGGCTTACCTCCAGTGTCAAGCATC 509  
 Qy 281 TCAACAATACAACTGTCATGGAAGAGATGGCACCATCCAGGACTCATATACCAAG 340  
 Db 510 TAAACAACCAAGTTGTTCTTGGAAACAAGATGGCATCTCCATGGAGTCAGATATCAGG 569  
 Qy 341 ACGGAACTGATAGTCCAAATCCCTGGCTTGTACTTTCATCGTTTGGCAACTGCAGTTCC 400  
 Db 570 ATGGAACTGATAGTCCAAATCCCTGGCTTGTACTTTCATCGTTTGGCAACTGCAGTTTC 629  
 Qy 401 TCGTCAGTGTCAATCATCTTCTGGACCTGACATTCAGCTCCTCATCAATTCAGA 460  
 Db 630 TTGTACAATGCCAAATAATTTCTGCGATCTGAAGTGGAGCTTCTCATCAACAAGCATA 689  
 Qy 461 TCAAAAACGACAGCTGTGTACAGTGTGTGAGTCTGGAGTTCAGAGTGAAGAATCTACC 520  
 Db 690 TCAAAAAMAGCCCTGGTGACAGTGTGTGAGTCTGGAGTGAAGAACAACAGTATACC 749  
 Qy 521 AGAATCTCTCAGTTTTTGTGTCATTACTTACAGGTCAACTCTTACCATATACAGTCAGG 580  
 Db 750 AGAATCTCTCAGTTTTTGTGTCATTACTTACAGGTCAACTCTTACCATATACAGTCAGT 809  
 Qy 581 TGGATAATTCAGTATGAGTATCAACAACATTTCCCTCTCTGATATGCTATCCGCT 640  
 Db 810 TGGATACATTCAGTATGAGTATCAACAACATTTCCCTCTCTGATATGCTATCCGCT 869  
 Qy 641 TCTATATAGTAGCTCAGACTGA 663  
 Db 870 TCTATACAGTAATTCAGACTGA 892

2



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ORIGIN
Query Match      56.0%; Score 371.6; DB 173; Length 634;
Best Local Similarity 92.0%; Pred. No. 9.2e-103;
Matches 392; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 82 CTCAGACACCGCACTGGTGTGCTTGTGGTGGAGTGGCGATCATCTGGTACTGGTA 141
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Db 634 CTAAGAACCCCGCAGTGGGTGCTTGTGGTGGCAGTGAGAATCATCTGGTCTGGTA 575
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QY 142 GTCAGAGAAAGACTCCACTCCAAATACAACTGAGAAGGCCCCCTTAAAGGAGGAAT 201
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QY 202 TGCTCAGAGGATCTCTCTGCTACCCCTGAAAGTACTCCATCCAAAGTATGATGGCCCTAC 261
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Db 214 CAGAGT 209

RESULT 4
BF890112 487 bp mRNA EST 18-JAN-2001
LOCUS 289772 MARC 3BOV Bos taurus cdna 5', mRNA sequence.
ACCESSION BF890112
VERSION BF890112.1 GI:12281570
KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 487)
AUTHORS Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
,W.W. and Keele,J.W.
Design and use of four pooled tissue normalized cdna libraries for
EST discovery in cattle
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACGATCAGCAGC
Plate: 96 row N column: 9
Seq primer: ATTTAGGTGACACTATAG.
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M.J., Soares.F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome

This sequence was derived from the FARESE7/LUDW human cancer genome project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=RC5-BT0559-140>)  
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BASE COUNT 80 a 63 c 56 g 78 t  
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327	ACTCATATACCGAGCGGGAACCTGATAGTCCAAATTCCTGGCTGTACTTCATCGTTTG	386		
1	AGTCAGATATCAGGATGGGAATCTGGTGATTCAAATCCCTGGTTGTACTTCATCAITTG	60		
387	C-CAACTGCAGATTCTCGTGCAGTGTCAAATCATTTCTGGACCTGACATTTGCAGCTCC	445		
61	CGCAACTGCAGTTTCTTGTGACAATGCCAAATAATCTGTGCGATCTGAAGTTGGAGCTTC	120		
446	TCATCAATTCACAGATCAAAAACGACAGTGTGGTAACAGTGTGTGAGTCTGGAGTTTCAGA	505		
121	TCATCAACAGGCATATCAAAAAACAGGCCCTGGTGACAGTGTGTGAGTCTGGAAATGCAAA	180		
506	GTAAGAACATCTACCAAGATCTCTCTCAGTTTTTGTCTGCATTTACTTACAGGTCAACTCTA	565		
181	CGAAACACGTATACCAAGATCTCTCAATTTCTGTGGATTACCTGCAGGTCAACACCA	240		
566	CCATATCAGTCAGGGTGGATAATTTCCAGT	595		
241	CCATATCAGTCAATGTGGATACATTTCCAGT	270		

[illegible]

LOCUS	AW654920	350 bp	mRNA	EST	
DEFINITION	105425 MARC Bos taurus cDNA 5',				EST
ACCESSION	AW654920				
VERSION	AW654920.1	GI:7420746			
KEYWORDS	EST.				
SOURCE	COW.				
ORGANISM	Bos taurus				
	Eukaryota;				
	Metazoa;				
	Chordata;				
	Craniata;				
	Vertebrata;				
	Euteleostomi;				
	Eutheria;				
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Best Local Similarity 55.2%; Pred. No. 0.022;
Matches 85; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
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Db 96 TCATCAAGCAGGTTCTGTAAAGTCCCACACCGGTCTAGTCTCTGGATAAAGTAACCG 155
QY 491 AGTCTGGAGTTCAGATAGACATCTACAGAAATCTCTCAGTTTTCGTCATTACT 550
Db 156 AGGATGGCGAGCATAGCCAGTCTATCGTTCTTGACCTCTTGAGTTTCAGCTCCTTCAGT 215
QY 551 TACAGGTCACACTACCATATCAGTCAGGTGGA 584
Db 216 GACTTCTCATCTTTCCCAACCAAGAGGGTTGA 249

RESULT 14
LOCUS      Z17941      271 bp      mRNA      EST      10-NOV-1992
DEFINITION ATTS0425 Strasbourg-A Arabidopsis thaliana cDNA clone SASFB04 5',
similar to Tomato type III chlorophyll a/b binding polypeptide of
photosystem I (Cab-8). GenBank entry X15258, mRNA sequence.
ACCESSION  Z17941
VERSION    Z17941.1 GI:17069
KEYWORDS   EST, thale cress.
SOURCE     Arabidopsis thaliana
ORGANISM   Arabidopsis thaliana
REFERENCE  1 (bases 1 to 271)
AUTHORS    CNRS.
TITLES     The Arabidopsis thaliana transcribed genome: the GDR cDNA program
JOURNAL    Unpublished (1996)
COMMENT    Contact: Parmentier Y., Criqui M.C., Durr A., Fleck J.
Fleck Jacqueline / 1626
Biologie Moleculaire des Plantes - CNRS
12 Rue du General Zimmer, 67084 Strasbourg Cedex, France
Email: ARABANK@MEDOC.U-STRASBG.FR.
FEATURES   Location/Qualifiers
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/strain="ecotype Columbia"
/db_xref="taxon:3702"
/clone="SASFB04"
/clone_lib="Strasbourg-A"
/note="Vector: Lambda ZAPII; tissue-sliced leaves of
A.thaliana ecotype columbia; clone_library-Strasbourg-A;
Cloning vector: Lambda ZAPII; Physiological condition:
leaves strips incubated 2/3/4 days in liquid culture
medium."
BASE COUNT      67 a   65 c   72 g   67 t
ORIGIN
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Best Local Similarity 53.9%; Pred. No. 0.21;

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Matches 83; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
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Db 228 TGATCAAGCAGGTTCTGTAAAGTCCCACACCGGTCTAGTCTCTGGATAAAGTAACCG 169
QY 491 AGTCTGGAGTTCAGATAGAACATCTACAGAAATCTCTCAGTTTTCGTCATTACT 550
Db 168 AGGATGGCGAGCATAGCCAGTCTATCGTTCTTGACCTCTTGAGTTTCAGCTCCTTCAGT 109
QY 551 TACAGGTCACACTACCATATCAGTCAGGTGGA 584
Db 108 GACTTCTCATCTTTCCCAACCAAGAGGGTTGA 75

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DEFINITION AV560475 Arabidopsis thaliana green siliques Columbia Arabidopsis
thaliana cDNA clone SQ135c06F 3', mRNA sequence.
ACCESSION  AV560475
VERSION    AV560475.1 GI:8731901
KEYWORDS   EST, thale cress.
SOURCE     Arabidopsis thaliana
ORGANISM   Arabidopsis thaliana
REFERENCE  1 (bases 1 to 277)
AUTHORS    Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLES     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
JOURNAL    DNA Res. 7, 175-180 (2000)
MEDLINE    20363093
COMMENT    Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizukazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
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XhoI"
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Best Local Similarity 53.9%; Pred. No. 0.21;
Matches 83; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
QY 431 TGACATTGCAGCTCCTCATCAATTCCAAGATCAAAAAGCAGACGTTGGTAACAGTGTG 490
Db 2 TGATCAAGCAGGTTCTGTAAAGTCCCACACCGGTCTAGTCTCTGGATAAAGTAACCG 61
QY 491 AGTCTGGAGTTCAGATAGAACATCTACAGAAATCTCTCAGTTTTCGTCATTACT 550
Db 62 AGGATGGCGAGCATAGCCAGTCTATCGTTCTTGACCTCTTGAGTTTCAGCTCCTTCAGT 121
QY 551 TACAGGTCACACTACCATATCAGTCAGGTGGA 584
Db 122 GACTTCTCATCTTTCCCAACCAAGAGGGTTGA 155

Search completed: September 6, 2001, 00:14:53

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 5, 2001, 21:55:46 ; Search time 68.95 Seconds  
(without alignments)  
1820.352 Million cell updates/sec

Title: US-09-628-126-18  
Perfect score: 663  
Sequence: 1 ATCAGGTGACCGCGCTC.....TATATAGTACTGACTGCA 663

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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10	402.2	60.7	648	1	US-08-570-923-22
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12	402.2	60.7	648	3	US-09-079-785-22
13	402.2	60.7	705	1	US-08-225-989-7
14	402.2	60.7	705	1	US-08-570-923-7
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17	34.2	5.2	1433	3	US-08-694-915-1
18	33.2	5.0	1501	2	US-08-145-6580-24
19	32	4.8	1526	1	US-08-694-915-3
20	31	4.7	180	6	5508199-1
21	31	4.7	1566	2	US-08-145-6580-13
22	31	4.7	1566	2	US-08-145-6580-22
23	31	4.7	1568	2	US-08-145-6580-20
24	31	4.7	1571	2	US-08-145-6580-21
25	30.8	4.6	2793	1	US-08-209-747-1
26	30.8	4.6	2793	1	US-08-458-298-1
27	30.6	4.6	1720	3	US-08-705-771-2

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30	30.4	4.6	1491	4	US-08-913-014A-5	Sequence 5, Appli
31	30.2	4.6	1480	3	US-09-090-793-4	Sequence 4, Appli
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33	29.4	4.4	1569	2	US-08-145-658D-23	Sequence 23, Appli
34	29.2	4.4	940	4	US-09-479-524-2	Sequence 2, Appli
35	29.2	4.4	940	4	US-09-479-524-8	Sequence 8, Appli
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ALIGNMENTS

RESULT 1  
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; Sequence 18, Application US/08225989  
; Patent No. 5480981  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5480981le1 Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644



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; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 663 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: mucD30-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..663
US-08-225-989-18

Query Match 100.0%; Score 663; DB 1; Length 663;
Best Local Similarity 100.0%; Pred. No. 2.4e-209;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 301 TGAACGAGATGGCACCATCCACGACTCATATACCAGGACGGAACTGATAGTCCAA 360
DB 301 TGAACGAGATGGCACCATCCACGACTCATATACCAGGACGGAACTGATAGTCCAA 360
QY 361 TTCCCTGGCTTGTACTTCATCGTTTGCACATGTCAGTTCCTGTCAGTGTCAAAATCAT 420
DB 361 TTCCCTGGCTTGTACTTCATCGTTTGCACATGTCAGTTCCTGTCAGTGTCAAAATCAT 420
QY 421 TCTGTGGACCTGACATTCAGTCTCCTCATCAATTCCAAGATCAAAAGCAGAGCTTGGTA 480
DB 421 TCTGTGGACCTGACATTCAGTCTCCTCATCAATTCCAAGATCAAAAGCAGAGCTTGGTA 480
QY 481 ACAGTGTGTAGTCTGGAGTTTCAGAGTGAAGACATCTACCAAGATCTCTCTCAGTTTTG 540
DB 481 ACAGTGTGTAGTCTGGAGTTTCAGAGTGAAGACATCTACCAAGATCTCTCTCAGTTTTG 540
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DB 541 CTGCATTACTTACAGGTCACCTTACCATATACATATCAGTTCAGGTGGATAATTTCCAGTATG 600
QY 601 GATACAACACTTTCCCTCTTGTATATGCTATCGTCTCTTATATAGTACGTCAGAC 660
DB 601 GATACAACACTTTCCCTCTTGTATATGCTATCGTCTCTTATATAGTACGTCAGAC 660
QY 661 TGA 663
DB 661 TGA 663

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RESULT 2

US-08-570-923-18

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; Sequence 18, Application US/08570923
; Patent No. 5677430
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,923
; FILING DATE: 12-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 663 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: mucD30-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..663
US-08-570-923-18

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Query Match 100.0%; Score 663; DB 1; Length 663;  
Best Local Similarity 100.0%; Pred. No. 2.4e-209; Indels 0; Gaps 0;  
Matches 663; Conservative 0; Mismatches 0;

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Db 61 ACAAGTCGAGCTACTTACCTACGACACCGCAGCTGGTGTGCTGTGGGAGTG 120  
Qy 121 GCGATCATCTGCTAGTCTGCTAGTCCAGAAAGAGTCCCAATACAACTGAGAAG 180  
Db 121 GCGATCATCTGCTAGTCTGCTAGTCCAGAAAGAGTCCCAATACAACTGAGAAG 180  
Qy 181 GCGCCCTTAAAGAGGAGAAATGCTCAGAGGATCTCTGTACCCCTGAAAGTACTCCA 240  
Db 181 GCGCCCTTAAAGAGGAGAAATGCTCAGAGGATCTCTGTACCCCTGAAAGTACTCCA 240  
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Db 241 TCCAGAAAGTATGAGGCTTACCTCCAAAGTGTCAAGCATCTCAACATACCAAACTGTCA 300  
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Db 301 TGAACGAAGATGGCAGCAGTCCAGGAGTATATACCAAGCGGAGCTGATAGTCCA 360  
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Db 361 TTCCCTGGCTTGTACTTCTGCTTTCGCAAGTCTGCTGCAAGTCTCAAAATCAT 420  
Qy 421 TCTGTGGACCTGACATTTGAGCTTCTCATCAATTTCAAGATCAAAAGAGAGCTTGGTA 480  
Db 421 TCTGTGGACCTGACATTTGAGCTTCTCATCAATTTCAAGATCAAAAGAGAGCTTGGTA 480  
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Db 481 ACAGTGTGAGTCTGAGTTCAGAGTCAAGATATACCAAGATCTCTCTCAGTATGTG 540  
Qy 541 CTGCATTACTTACAGTCAACTCTACCATATCATGAGTCTGAGTATATTTCCAGTATGTG 600  
Db 541 CTGCATTACTTACAGTCAACTCTACCATATCATGAGTCTGAGTATATTTCCAGTATGTG 600  
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Db 601 GATACAAACACTTTCCTCTTGATATGTGCTATCGCTTCTTATATAGTATAGTCTCAGAC 660  
Qy 661 TGA 663  
Db 661 TGA 663

RESULT 3  
US-08-580-014-18  
; Sequence 18, Application US/08580014  
; Patent No. 5753203  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jürgen  
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/580,014

; FILING DATE: 20-DEC-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 663 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; IMMEDIATE SOURCE:  
; CLONE: mUCD30-L  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..663  
; US-08-580-014-18

Query Match 100.0%; Score 663; DB 1; Length 663;  
Best Local Similarity 100.0%; Pred. No. 2.4e-209; Mismatches 0; Indels 0; Gaps 0;  
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGCAGGTGCAGCCGGCTCGGTAGCCAGCCCTGGAGAGCAGGAGGAGC 60  
Db 1 ATGCAGGTGCAGCCGGCTCGGTAGCCAGCCCTGGAGAGCAGGAGGAGC 60  
Qy 61 ACAAGTCGAGCTACTTACCTACGACACCGCAGCTGGTGTGCTGTGGGAGTG 120  
Db 61 ACAAGTCGAGCTACTTACCTACGACACCGCAGCTGGTGTGCTGTGGGAGTG 120  
Qy 121 GCGATCATCTGCTAGTCTGCTAGTCCAGAAAGAGTCCCAATACAACTGAGAAG 180  
Db 121 GCGATCATCTGCTAGTCTGCTAGTCCAGAAAGAGTCCCAATACAACTGAGAAG 180  
Qy 181 GCGCCCTTAAAGAGGAGAAATGCTCAGAGGATCTCTGTACCCCTGAAAGTACTCCA 240  
Db 181 GCGCCCTTAAAGAGGAGAAATGCTCAGAGGATCTCTGTACCCCTGAAAGTACTCCA 240  
Qy 241 TCCAGAAAGTATGAGGCTTACCTCCAAAGTGTCAAGCATCTCAACATACCAAACTGTCA 300  
Db 241 TCCAGAAAGTATGAGGCTTACCTCCAAAGTGTCAAGCATCTCAACATACCAAACTGTCA 300  
Qy 301 TGAACGAAGATGGCAGCAGTCCAGGAGTATATACCAAGCGGAGCTGATAGTCCA 360  
Db 301 TGAACGAAGATGGCAGCAGTCCAGGAGTATATACCAAGCGGAGCTGATAGTCCA 360

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QY 361 TTCCCTGGCTGTGACTGCTACATCGCTTCCCAACTGCACTGCTCTGTCGAGTGTCTCAAAATCAT 420
Db 361 TTCCCTGGCTGTGACTGCTACATCGCTTCCCAACTGCACTGCTCTGTCGAGTGTCTCAAAATCAT 420
QY 421 TCTGTGGAGCTGACATGTCAGCTCTCATCAATTCGAAGATCAAAAGACAGAGCTTGGTA 480
Db 421 TCTGTGGAGCTGACATGTCAGCTCTCATCAATTCGAAGATCAAAAGACAGAGCTTGGTA 480
QY 481 ACAGTGTGTGAGTCTGAGCTTTCAGAGTAAAGAACATCTACAGAAATCTCTCTCAGTCTTTTG 540
Db 481 ACAGTGTGTGAGTCTGAGCTTTCAGAGTAAAGAACATCTACAGAAATCTCTCTCAGTCTTTTG 540
QY 541 CTGCATTACTTACAGTCAACTCTACCATATCAGTCAGGTGGATATTTCCAGTATGTG 600
Db 541 CTGCATTACTTACAGTCAACTCTACCATATCAGTCAGGTGGATATTTCCAGTATGTG 600
QY 601 GATACAAACACATTTCCCTCTTGATATGTCATCGCTCTCTTATATAGTACTCAGAC 660
Db 601 GATACAAACACATTTCCCTCTTGATATGTCATCGCTCTCTTATATAGTACTCAGAC 660
QY 661 TGA 663
Db 661 TGA 663

RESULT 4
US-09-799-785-18
; Sequence 18, Application US/09079785
; Patent No. 6143869
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 6143869el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,785
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
```

```
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 663 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: mUCD30-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..663
; US-09-079-785-18

Query Match 100.0%; Score 663; DB 3; Length 663;
Best Local Similarity 100.0%; Pred. No. 2.4e-209;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCAGGTGCAGCCCGCTCGGTAGCCAGCCCTGGAGAACGACGAGGCCCTGGAGAACG 60
Db 1 ATGCAGGTGCAGCCCGCTCGGTAGCCAGCCCTGGAGAACGACGAGGCCCTGGAGAACG 60
QY 61 ACAAGTGCAGCTACTTCTACCTCAGCACCCACCCACTGGTGTGCTTGTGTGGCAGTG 120
Db 61 ACAAGTGCAGCTACTTCTACCTCAGCACCCACCCACTGGTGTGCTTGTGTGGCAGTG 120
QY 121 GCGATCATCTGCTGCTAGTGTGAGTCCAGAAAGAGCTCCACTCCAAATACAACTGAGAAG 180
Db 121 GCGATCATCTGCTGCTAGTGTGAGTCCAGAAAGAGCTCCACTCCAAATACAACTGAGAAG 180
QY 181 GCGCCCTTAAAGGAGGAAATGCTCAGAGATCTCTCTGTACCTGAAAGTACTCCA 240
Db 181 GCGCCCTTAAAGGAGGAAATGCTCAGAGATCTCTCTGTACCTGAAAGTACTCCA 240
QY 241 TCCAAAGAGTCAATGGGCTTACCTCCAAAGTGTCAAGATCTCAACAATACCAACTGTCA 300
Db 241 TCCAAAGAGTCAATGGGCTTACCTCCAAAGTGTCAAGATCTCAACAATACCAACTGTCA 300
QY 301 TGAACGAAGATGCGACCATCCAGGACTCATATACAGAGCGGGAACTGATAGTCCAA 360
Db 301 TGAACGAAGATGCGACCATCCAGGACTCATATACAGAGCGGGAACTGATAGTCCAA 360
QY 361 TTCCCTGGCTGTGACTTTCATCGTTTGGCAACTGCGAGTCTCTGTCAGTGTCTCAAAATCAT 420
Db 361 TTCCCTGGCTGTGACTTTCATCGTTTGGCAACTGCGAGTCTCTGTCAGTGTCTCAAAATCAT 420
QY 421 TCTGTGGACCTGACATTTGCAAGTCTCTCATCAATTCGAAGATCAAAAGACAGAGCTTGGTA 480
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Db 541 CTGCATTACTTACAGTCAACTCTACCATATCAGTCAGGTGGATATTTCCAGTATGTG 600
QY 601 GATACAAACACATTTCCCTCTTGATATGTCATCGCTCTCTTATATAGTACTCAGAC 660
Db 601 GATACAAACACATTTCCCTCTTGATATGTCATCGCTCTCTTATATAGTACTCAGAC 660
QY 661 TGA 663
Db 661 TGA 663
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RESULT 5  
US-08-225-989-5  
; Sequence 5, Application US/08225989  
; Patent No. 5480981  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: NO. 5480981el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 720 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; IMMEDIATE SOURCE:  
; CLONE: muCD30-L  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..720  
; US-08-225-989-5

Query Match 100.08; Score 663; DB 1; Length 720;  
Best Local Similarity 100.08; Pred. No. 2.5e-209;  
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 ACAAAGTCGACGACTACTTCTACCTCAGCAGCACCACCGCAGCTGGTGTGCTTGTGTCAGTG 120  
DB 118 ACAAAGTCGACGACTACTTCTACCTCAGCAGCACCACCGCAGCTGGTGTGCTTGTGTCAGTG 177  
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QY 601 GATACAAACACTTCCCTCTTGATAATGCTATCCGCTCTTCTTATATAGTACGTCAGAC 660  
DB 658 GATACAAACACTTCCCTCTTGATAATGCTATCCGCTCTTCTTATATAGTACGTCAGAC 717  
QY 661 TGA 663  
DB 718 TGA 720

RESULT 6  
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; Sequence 5, Application US/08570923  
; Patent No. 5677430  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/570,923  
;; FILING DATE: 12-DEC-1995  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/225,989  
;; FILING DATE: 12 APRIL 1994  
;; APPLICATION NUMBER: US 07/966,775  
;; FILING DATE: 27-OCT-1992  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 907,224  
;; FILING DATE: 01-JUL-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 899,660  
;; FILING DATE: 15-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 892,459  
;; FILING DATE: 02-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 889,717  
;; FILING DATE: 26-MAY-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Seese, Kathryn A.  
;; REGISTRATION NUMBER: 32,172  
;; REFERENCE/DOCKET NUMBER: 2804-E  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206)587-0430  
;; TELEFAX: (206)233-0644  
;; TELEX: 756822  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 720 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA to mRNA  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; IMMEDIATE SOURCE:  
;; CLONE: mUCD30-L  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 1..720  
;; US-08-570-923-5

Query Match 100.0%; Score 663; DB 1; Length 720;  
Best Local Similarity 100.0%; Pred. No. 2.5e-209;  
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGACAGTGCAGCCGGCTCGGTAGCCAGCCCTGGAGAACGACGAGGCCCTGGAGAAGC 60  
Db 58 ATGACAGTGCAGCCGGCTCGGTAGCCAGCCCTGGAGAACGACGAGGCCCTGGAGAAGC 117  
QY 61 ACAAGTGCAGCTACTTCTACTCAGCACCACCGACCTGGTGTGCTGTGTCGCGAGTG 120  
Db 118 ACAAGTGCAGCTACTTCTACTCAGCACCACCGACCTGGTGTGCTGTGTCGCGAGTG 177  
QY 121 CGCATCATTTCTGGTGTAGTCCAGAAAAAGGACTCCACTCCCAAAATACAACTGAGAAG 180  
Db 178 CGCATCATTTCTGGTGTAGTCCAGAAAAAGGACTCCACTCCCAAAATACAACTGAGAAG 237  
QY 181 GCCCCCTTAAAGGAGGAAATGTCAGAGGATCTCTTCTGTACCTGAAAGTACTCCA 240  
Db 238 GCCCCCTTAAAGGAGGAAATGTCAGAGGATCTCTTCTGTACCTGAAAGTACTCCA 297  
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Db 298 TCCAGAGTCAATGGCCCTACTCCAGTGTCAAGCATCTCAACAAATACCAAACTGTCA 357  
QY 301 TGGAAACGAAGTGCACCATCCAGGACTCATATACGAGGAGGGAACCTGATAGTCCAA 360  
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Db 358 TGGAAACGAAGTGCACCATCCAGGACTCATATACGAGGAGGGAACCTGATAGTCCAA 417  
QY 361 TTCCCTGGCTTGTACTTCATCGTTTGCCAACTGCAGTTCCCTCGTGCGAGTGTCAAATCAT 420  
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Db 418 TTCCCTGGCTTGTACTTCATCGTTTGCCAACTGCAGTTCCCTCGTGCGAGTGTCAAATCAT 477  
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QY 421 TCTGTGGACCTGCATTTGCAGCTCCTCATCAATTCCTCAAGATCAAAAAAGCAGACGTTGGTA 480  
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Db 478 TCTGTGGACCTGCATTTGCAGCTCCTCATCAATTCCTCAAGATCAAAAAAGCAGACGTTGGTA 537  
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QY 481 ACAGTGTGTGAGTCTGGAGTTTCAGAGTAAGAACAATCTACCAAGATCTCTCTCAGTTTTTG 540  
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Db 538 ACAGTGTGTGAGTCTGGAGTTTCAGAGTAAGAACAATCTACCAAGATCTCTCTCAGTTTTTG 597  
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QY 541 CTGCATTACTTACAGGTCAACTCTTACCATATCAGTCAAGGTGGATAATTTCCAGTATGTG 600  
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Db 598 CTGCATTACTTACAGGTCAACTCTTACCATATCAGTCAAGGTGGATAATTTCCAGTATGTG 657  
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QY 601 GATACAAACACTTTCCCTCTTGATAATGTGCTATGCCCTCTTCTTATATAGTAGTCTCAGAC 660  
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Db 658 GATACAAACACTTTCCCTCTTGATAATGTGCTATGCCCTCTTCTTATATAGTAGTCTCAGAC 717  
QY 661 TGA 663  
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Db 718 TGA 720  
|||||  
RESULT 7  
US-08-580-014-5  
; Sequence 5, Application US/08580014  
; Patent No. 5753203  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/580,014  
; FILING DATE: 20-DEC-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 720 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: mucD30-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..720  
US-08-580-014-5

Query Match 100.0%; Score 663; DB 1; Length 720;  
Best Local Similarity 100.0%; Pred. No. 2.5e-209; Indels 0; Gaps 0;  
Matches 663; Conservative 0; Mismatches 0;

QY 1 ATGCAGTGCAGCCGGCTCGGTAGCCAGCCCTGGAGAGCAGCAGGCCCTGGAGAGC 60  
DB 58 ATGCAGTGCAGCCGGCTCGGTAGCCAGCCCTGGAGAGCAGCAGGCCCTGGAGAGC 117  
QY 61 ACAAGTCGAGCTACTTCTACCTCAGCACCCGCACTGGTGTGCTTGTGTGGCAGTG 120  
DB 118 ACAAGTCGAGCTACTTCTACCTCAGCACCCGCACTGGTGTGCTTGTGTGGCAGTG 177  
QY 121 GCGATCATTTCTGTACTGGTAGTCCAGAAAAGAGCTCCACTCCAATACAACTGAGAAG 180  
DB 178 GCGATCATTTCTGTACTGGTAGTCCAGAAAAGAGCTCCACTCCAATACAACTGAGAAG 237  
QY 181 GCCCCCTTTAAAGGAGAAATTCCTCAGAGGATCTCTCTGTACCCCTGAAAGTACTCCA 240  
DB 238 GCCCCCTTTAAAGGAGAAATTCCTCAGAGGATCTCTCTGTACCCCTGAAAGTACTCCA 297  
QY 241 TCCAGAGTCAATGGCCCTACCTCCCAAGTGTCAAGCATCTCAACAACTGCTCA 300  
DB 298 TCCAGAGTCAATGGCCCTACCTCCCAAGTGTCAAGCATCTCAACAACTGCTCA 357  
QY 301 TGGAAACAGATGGCACCACCTCCAGGACTCATATACCAGGACGGGAACCTGATAGTCAA 360  
DB 358 TGGAAACAGATGGCACCACCTCCAGGACTCATATACCAGGACGGGAACCTGATAGTCAA 417  
QY 361 TTCCTCGGCTGTGACTTTCCTGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
DB 418 TTCCTCGGCTGTGACTTTCCTGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 477  
QY 421 TCTGTGGACCTGACATTCGAGCTTCTCATCAATTCGAAGATCAAAAGACGACGCTTGCTA 480  
DB 478 TCTGTGGACCTGACATTCGAGCTTCTCATCAATTCGAAGATCAAAAGACGACGCTTGCTA 537  
QY 481 ACAGTGTGAGTCTGGAGTTCAGAGTGAAGACATCTACAGAACTCTCTCTCAGTCTTTTG 540  
DB 538 ACAGTGTGAGTCTGGAGTTCAGAGTGAAGACATCTACAGAACTCTCTCTCAGTCTTTTG 597  
QY 541 CTGCATTACTACAGTCAACTTACCATCATCATGAGGCTGATATTTCCAGTATGTG 600  
DB 598 CTGCATTACTACAGTCAACTTACCATCATCATGAGGCTGATATTTCCAGTATGTG 657  
QY 601 GATACAAACACTTTCCTCTTGTATATGTCTATCCGCTCTCTTATATAGTACGCTCAGAC 660  
DB 658 GATACAAACACTTTCCTCTTGTATATGTCTATCCGCTCTCTTATATAGTACGCTCAGAC 717  
QY 661 TGA 663

Db 718 TGA 720  
RESULT 8  
US-09-079-785-5  
Sequence 5, Application US/09079785  
Patent No. 6143869  
GENERAL INFORMATION:  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
APPLICANT: Armitage, Richard J.  
APPLICANT: Gruss, Hans-Jurgen  
TITLE OF INVENTION: No. 6143869el Cytokine That Binds CD30  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,785  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,989  
FILING DATE: 12 APRIL 1994  
APPLICATION NUMBER: US 07/966,775  
FILING DATE: 27-OCT-1992  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 720 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: mucD30-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..720  
US-09-079-785-5

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Query Match 100.0%; Score 663; DB 3; Length 720;
Best Local Similarity 100.0%; Pred. No. 2.5e-209;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCAGGTGACAGCCCGCTCGGTAGCCAGCCCTGGAGAGACGAGGCGCTGGAGAAGC 60
DB 58 ATGCAGGTGACAGCCCGCTCGGTAGCCAGCCCTGGAGAGACGAGGCGCTGGAGAAGC 117
QY 61 ACAAGTCGCGAGTACTTCTACCTCAGCACCACCGCACTGGTGCGCTTGTGTGGCAGTG 120
DB 118 ACAAGTCGCGAGTACTTCTACCTCAGCACCACCGCACTGGTGCGCTTGTGTGGCAGTG 177
QY 121 GCGATCATTCTGGTACTGTAGTCCAGAAAAAGGACTCCCACTCCAATACAACCTGAGAAG 180
DB 178 GCGATCATTCTGGTACTGTAGTCCAGAAAAAGGACTCCCACTCCAATACAACCTGAGAAG 237
QY 181 GCCCCCCCTAAAGGAGGAATGTCTCAGAGGATCTCTCTGACCCCTGAAAAGTACTCCA 240
DB 238 GCCCCCCCTAAAGGAGGAATGTCTCAGAGGATCTCTCTGACCCCTGAAAAGTACTCCA 297
QY 241 TCCAAAGAGTCAATGGCCCTACCTCCCAAGTGTCAAAGCATCTCAACAATACCAAACTGTCA 300
DB 298 TCCAAAGAGTCAATGGCCCTACCTCCCAAGTGTCAAAGCATCTCAACAATACCAAACTGTCA 357
QY 301 TGGAAAGAGTGGCACCACATCCAGGACTCATATACGAGGCGGGAACCTGATAGTCCAA 360
DB 358 TGGAAAGAGTGGCACCACATCCAGGACTCATATACGAGGCGGGAACCTGATAGTCCAA 417
QY 361 TTCCTGGCTGTACTTCATCGTTTGCCAACTGCAAGTCTCTGTCAGTGCCTCAAAATCAT 420
DB 418 TTCCTGGCTGTACTTCATCGTTTGCCAACTGCAAGTCTCTGTCAGTGCCTCAAAATCAT 477
QY 421 TCTGTGGACCTGACATTCGAGCTCTCTCATCAATTCGAAGATCAAAAGCAGAGCTGGTA 480
DB 478 TCTGTGGACCTGACATTCGAGCTCTCTCATCAATTCGAAGATCAAAAGCAGAGCTGGTA 537
QY 481 ACAGTGTGTGAGTGTGGAGTTCAGAGTAGAAGATCTACCAAGATCTCTCAGTGTGG 540
DB 538 ACAGTGTGTGAGTGTGGAGTTCAGAGTAGAAGATCTACCAAGATCTCTCAGTGTGG 597
QY 541 CTGCAATTACTTACAGGTCAACTCTACCATATCAGTCAGGCTGGATTAATTTCCAGTATGTG 600
DB 598 CTGCAATTACTTACAGGTCAACTCTACCATATCAGTCAGGCTGGATTAATTTCCAGTATGTG 657
QY 601 GATACAAACACTTTCCCTCTTGATATGTGCTATCGCTCTCTTATATAGTACGCTCAGAC 660
DB 658 GATACAAACACTTTCCCTCTTGATATGTGCTATCGCTCTCTTATATAGTACGCTCAGAC 717
QY 661 TGA 663
DB 718 TGA 720

RESULT 9
US-08-225-989-22
; Sequence 22, Application US/08225989
; Patent No. 5480981
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Amittage, Richard J.
; APPLICANT: Gruss, Hans-Jürgen
; TITLE OF INVENTION: No. 3480981el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; IMMEDIATE SOURCE:
; CLONE: huCD30-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..648
; US-08-225-989-22

Query Match 60.7%; Score 402.2; DB 1; Length 648;
Best Local Similarity 79.0%; Pred. No. 3.3e-123;
Matches 492; Conservative 0; Mismatches 128; Indels 3; Gaps 1;

QY 44 CGAGGCCCTGGAGAGCAGACAAAGTCGCGAGCTACTTCTACCTCAGGACCAACCGCACTGG--- 100
DB 26 CCAGCCACCTGGGGACCAACGAGCGCGCAGCTATTCTATTGACCACAGCCACTCTGGCTC 85
QY 101 TGTGCTCTGTGTGGGAGTGGCGATCATCTGTGCTAGTGTAGTCCAGAGAAAGACTCCA 160
DB 86 TGTGCTCTGTGTGGGAGTGGCGATCATCTATTATGTTGTTGCTCAGAGAGCGACTCCA 145
QY 161 CTCCAATACAACTGAGAGGCGCCCTTAAAGGAGGAAATGTCTCAGAGGATCTCTTCT 220
DB 146 TTCCCAACTCACTGACACAGTCCCTTCAAGAGGAGAAATGCTCAGAGAGCTCTTAT 205
QY 221 GTACCTGAAAGTACTTCCATCCAAGAAAGTCATGGGCTTACCTCCCAAGTGTCAAGATC 280
DB 206 GTATCTGAAAGAGGTCCATTCGAAGAAGTCATGGGCTTACCTCCCAAGTGTCAAGATC 265
QY 281 TCAACAATACCAACTCTCATGGAACGAGATGCAACCATCCAGGACTCATATACAGG 340
DB 266 TAAACAAACCAAGTGTCTTGGAAACAAAGATGCAATTCCTCATGAGTGCAGATATCAGG 325
QY 341 ACGGGAACCTGATAGTCCCAATTCCTGGCTTGACTTCTATCTGTTGCAACTGCAGTTCC 400
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Db 326 ATGGGAATCTGGTGATCCAAATCCCTGGTTGTGTACTTCAATTTGCCAACTCAGTTTC 385  
Qy 401 TCGTCAGTGTCAAAATCAATTCCTGGAGCTGCATTTGAGCTCCCTCATCAATTTCCAGA 460  
Db 386 TTGTACAATGCCCAATAAATTTCTGCTGATCTGAAGTTGGAGCTTCTCATCAACAAGATA 445  
Qy 461 TCAAAAAGCAGACGCTGGTAAACAGTGTGTGAGTCTGAGTTCAGAGTTCAAGAACATCTACC 520  
Db 446 TCAAAAAGCAGCCCTGGTGACAGTGTGTGAGTCTGGAATGCAAAACGAAACAGTATACC 505  
Qy 521 AGAATCTCTCAGTCTTTTGGCTGCAATTTACAGTCAACTCTACCATATCAGTCAGG 580  
Db 506 AGAATCTCTCAATTTCTGCTGGATTACTCTGAGTCAACACCACTATCAGTCAATG 565  
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Db 626 TCTTATACAGTAATTCAGACTGA 648

RESULT 10  
US-08-570-923-22  
; Sequence 22, Application US/08570923  
; Patent No. 5677430  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/570,923  
; FILING DATE: 12-DEC-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 648 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; IMMEDIATE SOURCE:  
; CLONE: huCD30-L  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..648  
; US-08-570-923-22

Query Match 60.7%; Score 402.2; DB 1; Length 648;  
Best Local Similarity 79.0%; Pred. No. 3.3e-123;  
Matches 492; Conservative 0; Mismatches 128; Indels 3; Gaps 1;

Qy 44 CGAGGCCTCGAGAAGCACAAAGTCGACGTACTTCTACTCGACACACCGCAGCTGG--- 100  
Db 26 CCAGCCACTGGGACCCAGAGCCGACGCTATTCTATTGACCACGCCACTCTGGGTC 85  
Qy 101 TGTGCTTGTGTGGCAGTGGCGATCATTTCTGGTACTGTGTATGCCAGAAAAAGGACTCCA 160  
Db 86 TGTGCTTGTCTTCAGGGTGGCCACTATTATGTTGTTGTTGTTTCAGAGGAGGACTCCA 145  
Qy 161 CTCGAATACAACTGAGAAGGCCCCCTTAAAGGAGGAAATTCGTCAGAGGATCTCTTCT 220  
Db 146 TTCCCAACTCACCTGACACGCTCCCTTCAAGGAGGAAATTCGTCAGAGGACCTCTTAT 205  
Qy 221 GTACCTCAAAAGTACTCCATCCAAAGAGTCATGGCCCTACTCCCAAGTGTCAAGAGCATC 280  
Db 206 GTATCTGAAAAGAGCTCCATTCAAAGAGTCATGGGCCCTACTCCCAAGTGGCAAGCATC 265  
Qy 281 TCAACAATACCAAACTGTCTATGGACGAGAGATGGCACCATCCAGGACTCATATACCAAG 340  
Db 266 TAACAAAACCAAGTTGCTTTGGAACAAGATGGCATTTCCATGGAGTCAGATATCAGG 325  
Qy 341 ACAGGAACCTGATAGTCCAAATTCCTGGCTGTGACTTTCATCGTTGGCAACTGCAAGTCC 400  
Db 326 ATGGGAATCTGGTGATCCAAATTCCTGGTTGTACTTTCATCATTTGCCAACTGCAAGTTTC 385  
Qy 401 TCGTGCAGTGTCTCAAAATCATTTCTGTGGACCTGACATTCGAGCTCTCTCATCAATTCAGA 460  
Db 386 TTGTACAATGCCCAAAATAATTTCTGCGATCTGAAGTTGGAGCTTCTCATCAACAAGCAT 445  
Qy 461 TCAAAAAGCAGACGTTGGTAAACAGTGTGTGAGTCTGGAGTTCCAGAGTAAGAACATCTACC 520  
Db 446 TCAAAAACAGCCCTGGTGACAGTGTGTGAGTCTGGAGTAAGAACGAAACACGATATACC 505  
Qy 521 AGAATCTCTCAGTCTTTTGTGCTGCAATTTACAGGTCACACTTACCATATATCAGCAGG 580  
Db 506 AGAATCTCTCAATTTCTGCTGGATTACCTGCGAGTCAACACCACTATCAGTCAATG 565  
Qy 581 TGGATAATTTCCAGTATGTGGATACAAACACTTTCCCTCTTTGATAATGTCTATCCGTCT 640  
Db 566 TGGATACATTTCCAGTACATAGATACAAAGCACTTTCTCTTCTTGGAGATGTGTGTCATCT 625  
Qy 641 TCTTATATAGTACCTCAGACTGA 663  
Db 626 TCTTATACAGTAATTCAGACTGA 648

RESULT 11  
US-08-580-014-22  
; Sequence 22, Application US/08580014  
; Patent No. 5753203  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.



APPLICANT: Smith, Craig A.  
 APPLICANT: Armitage, Richard J.  
 APPLICANT: Gruss, Hans-Jurgen  
 TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
 STREET: 51 University Street  
 CITY: Seattle  
 STATE: Washington  
 COUNTRY: USA  
 ZIP: 98101  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: Apple Macintosh  
 OPERATING SYSTEM: Apple 7.1  
 SOFTWARE: Microsoft Word, Version 5.1a  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/580,014  
 FILING DATE: 20-DEC-1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/225,989  
 FILING DATE: 12 APRIL 1994  
 APPLICATION NUMBER: US 07/966,775  
 FILING DATE: 27-OCT-1992  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 907,224  
 FILING DATE: 01-JUL-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 899,660  
 FILING DATE: 15-JUN-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 892,459  
 FILING DATE: 02-JUN-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 889,717  
 FILING DATE: 26-MAY-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seese, Kathryn A.  
 REGISTRATION NUMBER: 32,172  
 REFERENCE/DOCKET NUMBER: 2804-E  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206)587-0430  
 TELEFAX: (206)233-0644  
 TELEX: 756822  
 INFORMATION FOR SEQ ID NO: 22:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 648 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 IMMEDIATE SOURCE:  
 CLONE: hucd30-L  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..648  
 PS-08-580-014-22

	Query Match	60.7%;	Score 402.2;	DB 1;	Length 648;
	Best Local Similarity	79.0%;	Pred. No. 3.3e-123;		
	Matches 492;	Conservative 0;	Mismatches 128;	Indels 3;	Gaps 1;
QY	44	CGAGGCCCTGGAGAAGCACAAAGTCGACGTACTTCTTACTCAGCACACCACGCACATGG---	100		
Db	26	CCAGCCCACTGGGACACCAGCGCGAGCTATTCTATTTCAGCCACACGCCACTCTGGCTC	85		
QY	101	TGTGCCCTTTGTGGCAGTGCGCATCATTTCTGGTACTGGTAGTCACAAAAAGGAACCTCCA	160		
Db	86	TGTGCCCTTTGCTTCACCGTGCCCACTAATAATGTTGGTGGTCTGTTCAGAGGACGGATCCA	145		

Qy	161	CTCAAAATACAACTGAGAGGCCCCCTTAAAGAGGAAATTTGCTCAGAGGATCTCTTCT	220
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	146	TTCCCAACTCACCTGACAACGTCCTCCCTCAAAGAGGAAATTTGCTCAGAAGACCTCTTAT	
Qy	221	GTACCTTGAAAGATCTCCCATCCCAAGAAGTCATGGGCCTACCTCCCAAGTGTCAAAGCATC	280
Db	206	TTTTTTTTT TTTTTTTTT TTTTTTTTT TTTTTTTTT TTTTTTTTT TTTTTTTTT	265
	206	GTATCTCTGAAAGAGCTCCATTTCAAGAAGTCATGGGCCTACCTCCCAAGTGGCAAAGCATC	
Qy	281	TCAACAATACCAAACTGTCTATGGAACCAAGATGGCACTCCACGGACTCATATACCAAG	340
Db	266	TTTTTTTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT	325
	266	TAAACAACAACCAAGTGTCTTGGAAACAAGATGGCATTTCCATGGAGTCAGATATCAGG	
Qy	341	ACGGGAACCTGATAGTCCAAATTCCTGGCTTGTACTTTCATCGTTTGGCAACTGCAGTTC	400
Db	326	TTTTTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT	385
	326	ATGGAAATCTGGTCATCCAAATTCCTTGTTTGTACTTTCATCATTTTGGCAACTGCAGTTTC	
Qy	401	TCGTGCAGTGTCCAAATCATTTCTGTGGACCTGACATTTGCAGCTTCCTCATCAATTCACA	460
Db	386	TTTTTTTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT	445
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RESULT 12  
 US-09-079-785-22  
 ; Sequence 22, Application US/09079785  
 ; Patent No. 6143869  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Goodwin, Raymond G.  
 ; APPLICANT: Smith, Craig A.  
 ; APPLICANT: Armitage, Richard J.  
 ; APPLICANT: Gruss, Hans-Jürgen  
 ; TITLE OF INVENTION: No. 6143869el Cytokine That Binds CD30  
 ; NUMBER OF SEQUENCES: 23  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
 ; STREET: 51'University Street  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; COUNTRY: USA  
 ; ZIP: 98101  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: Apple Macintosh  
 ; OPERATING SYSTEM: Apple 7.1  
 ; SOFTWARE: Microsoft Word, Version 5.1a  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/079,785  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/225,989  
 ; FILING DATE: 12 APRIL 1994  
 ; APPLICATION NUMBER: US 07/966,775  
 ; FILING DATE: 27-OCT-1992  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 907,224

FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 648 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
IMMEDIATE SOURCE:  
CLONE: huCD30-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..648  
US-09-079-785-22

Query Match 60.7%; Score 402.2; DB 3; Length 648;  
Best Local Similarity 79.0%; Pred. No. 3 3e-123;  
Matches 492; Conservative 0; Mismatches 128; Indels 3; Gaps 1;  
QY 44 CGAGCCCTGGAGACGACAGTCGAGCTACTTCTACCTCAGCAGCCGCGACTGG--- 100  
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QY 101 TGTGCTTTGTTGGCAGTGGGGATCTTCTGGTACTGGTAGTCCAGAAAAAGGACTCCA 160  
DB 86 TGTGCTTTGTTCTTCAGGTGGGCACTATTATGGTGTGTGCTGTCAGAGCGAGCTCCA 145  
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QY 221 GTACCTGAAAGTACTCCATCCAGAACTCATGGGCTTACCTCCAAAGTGTCAAAGCATC 280  
DB 206 GTATCCTGAAAGAGCTCCATTCAAGAGTCATGGGCTTACCTCCAAAGTGGCAAGCATC 265  
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QY 341 ACGGAACCTGATAGTCCAAATTCCTCGGCTTGTACTTCATCTGTTGCCAACTCAGTTCC 400  
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QY 461 TCAAAAGCAGACGTTGGTAAACAGTGTGAGTGTGAGTTTCAGAGTAAAGAACATCTACC 520  
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QY 521 AGAATCTCTCAGTTTGTGTCATTTACTTACAGGTCAACTTACCATATCATGTCAGG 580  
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QY 641 TCTTATAGTAGTCTCAGACTGA 663  
DB 626 TCTTATACAGTAATTCAGACTGA 648  
RESULT 13  
US-08-225-989-7  
Sequence 7, Application US/08225989  
Patent No. 5480981  
GENERAL INFORMATION:  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
APPLICANT: Armitage, Richard J.  
APPLICANT: Gruss, Hans-Jurgen  
TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,989  
FILING DATE: 12 APRIL 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/966,775  
FILING DATE: 27-OCT-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 705 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
IMMEDIATE SOURCE:  
CLONE: huCD30-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..705  
US-08-225-989-7

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; SOFTWARE: Microsoft Word, Version 5.1a
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; APPLICATION NUMBER: US/08/570,923
; FILING DATE: 12-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; IMMEDIATE SOURCE:
; CLONE: huCD30-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
; US-08-570-923-7

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Query Match 60.7%; Score 402.2; DB 1; Length 705;
Best Local Similarity 79.0%; Pred. No. 3.5e-123;
Matches 492; Conservative 0; Mismatches 128; Indels 3; Gaps 1;

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Qy 161 CTCCTCAATACAACTGAGAGGCGGCGGCTTTAAAGGAGGAAATGCTCAGAGGATCTCTTCT 220
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Db 323 TAAACAACCAAGTGTCTTGGACAAAGATGCGATTTCTCCATGGAGTCAAGATCAGG 382
Qy 341 ACGGGAACCTGATAGTCCAAATTCCTGGCTGTGTACTGTGTACTGTGTGTGTGTGTGTGTGT 400
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RESULT 14
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; Sequence 7, Application US/08570923
; Patent No. 5677430
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jürgen
; TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 5, 2001, 23:43:12 ; Search time 111.92 Seconds  
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Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	663	100.0	720	19	AAV42207
3	663	100.0	1783	19	AAV42186
4	661.4	99.8	720	14	AAQ53537
5	402.2	60.7	648	14	AAQ53536
6	402.2	60.7	705	14	AAQ53538
7	402.2	60.7	1906	19	AAV39012
8	42.6	6.4	936	22	AAF58252
9	42.6	6.4	936	22	AAF58252
10	42.6	6.4	936	22	AAF58254
11	42.6	6.4	936	22	AAF58254

12	42.6	6.4	936	22	AAF58257	Oligonucleotide D1
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16	42.6	6.4	936	22	AAF58262	Oligonucleotide D2
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18	42.6	6.4	938	22	AAF58255	Oligonucleotide D1
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21	40.4	6.1	1100	21	AAC49976	Arabidopsis thalia
22	38.8	5.9	1036	21	AAC36192	Arabidopsis thalia
23	38.8	5.9	1105	21	AAC37173	Arabidopsis thalia
24	38.8	5.9	1342	21	AAC52167	Arabidopsis thalia
25	34.4	5.2	4356	16	AAQ95540	Cardiac adenylyl c
26	34.2	5.2	379	21	AAC00135	Human secreted pro
27	34.2	5.2	1432	19	AAV21689	DNA encoding a hum
28	34.2	5.2	1433	19	AAV13925	Human cartilage gp
29	34.2	5.2	1496	18	AAV97127	Human cartilage gl
30	33.6	5.1	509	21	AAC08862	Human secreted pro
31	33.4	5.0	1886	22	AAF92535	Rat T2R08 nucleoti
32	33.2	5.0	3768	21	AAC81955	Human Meg-3 cDNA
33	32.8	4.9	1403	21	AAC36591	Arabidopsis thalia
34	32.8	4.9	4356	14	AAQ37543	Cardiac adenylyl c
35	32.4	4.9	1038602	20	AAZ01425	Complete genome se
36	32.2	4.9	1467	21	AAC78872	Human ORF2427
37	32	4.8	1526	19	AAV13926	Human cartilage gp
38	32	4.8	1594	19	AAV21687	DNA encoding a hum
39	32	4.8	1594	19	AAV21688	DNA encoding a hum
40	32	4.8	26016	19	AAV57272	Human flavin-conta
41	31.4	4.7	1205	22	AAC85551	cDNA encoding CDIF
42	31.4	4.7	1314	21	AAC44675	zea mays DNA fragm
43	31.2	4.7	374	21	AAA51168	Hybrid 7 transmemb
44	31.2	4.7	3428	19	AAV24138	Homo sapiens BAP15
45	31.2	4.7	3517	19	AAV18626	Homo sapiens BRCA1

## ALIGNMENTS

RESULT 1  
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ID AAQ53535 standard; cDNA; 663 BP.  
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AC AAQ53535;  
XX  
DT 19-JUN-1994 (first entry)  
XX  
DE Sequence of the coding region of a murine CD30-L cDNA clone.  
XX  
KW Hodgkin's disease; lymphoma; surface antigen; cytokine;  
XX CD30 ligand; CD30-L; TNF; NGF; ss.  
XX  
OS Acomys cahirinus.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..663  
FT /\*tag= a  
XX  
PN WO9324135-A.  
XX  
PD 09-DEC-1993.  
XX  
PF 25-MAY-1993; 93WO-US04926.  
XX  
PR 26-MAY-1992; 92US-0889717.  
XX 02-JUN-1992; 92US-0892459.  
PR 15-JUN-1992; 92US-0899660.  
PR 01-JUL-1992; 92US-0907224.  
PR 27-OCT-1992; 92US-0966775.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Armitage RJ, Goodwin RG, Smith CA;

QY	1	ATCAGGTGCAGCCCGCTCGGTAGCCAGCCCTGGAGAGACGACGAGCCCTGGAGAACG	60
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 QY 661 TGA 663  
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 Db 718 tga 720

## RESULT 3

AAV42186  
 ID AAV42186 standard; DNR; 1783 BP.

XX AC

AAV42186;

XX DT 23-SEP-1998 (first entry)

XX DE CD40 ligand gene used in the course of the invention.

XX KW CD40 ligand; alteration; immunoreactivity; human cell;  
 KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;  
 KW autoimmune disorder; rheumatoid arthritis; vaccine; ss.

XX OS Mus sp.

XX PN W09826061-A2.

XX PD 18-JUN-1998.

XX PF 08-DEC-1997; 97WO-US22740.

XX PR 01-DEC-1997; 97US-0982272.

XX PR 09-DEC-1996; 96US-0032145.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Cantwell M, Kipps TJ, Sharma S;

XX WPI; 1998-348521/30.

XX PT Vectors containing accessory molecule ligand genes - used for  
 PT altering immunoreactivity of cells, particularly for treatment of  
 PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis

XX PS Disclosure; Page 117; 167pp; English.

XX CC The present sequence represents a CD40 ligand gene. The sequence is  
 CC used to exemplify the method of the invention. The specification

CC describes a method for altering the immunoreactivity of human cells  
 CC which comprises introducing a gene encoding an accessory molecule  
 CC ligand (AML) into the cells so that the AML is expressed on the surface  
 CC of the cells. Vectors containing the AML genes can be used in gene  
 CC therapy for treating neoplasia or autoimmune disorders such as rheumatoid  
 CC arthritis. They can also be used for vaccination to produce immunity  
 CC against a virus cell, bacteria, protein, fungus or neoplasia.

XX SQ Sequence 1783 BP; 515 A; 411 C; 407 G; 450 T; 0 other;

Query Match 100.0%; Score 663; DB 19; Length 1783;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-200;  
 Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 350 gccccccttaagaggagaaattgctcagaggatctctctgtacctctgaaagactactcca 409  
 |||||||  
 QY 241 TCCAAGAGTCATGGGCTTACCTCCAAGTGTCAAAAGCATCTCAACAATACCAAACTGTCA 300  
 |||||||  
 Db 410 tccaagaagtcattgggcttacctccaagtgcaaaagcatctcaacaataccaaactgtca 469  
 |||||||  
 QY 301 TGGACGAAGATGCGACATCCACGGACTCATATACCAGGACGGGAACCTGATAGTCAA 360  
 |||||||  
 Db 470 tggaaagaagatggcaccatccacggactcatataccagagacggggaacctgatagtcaca 529  
 |||||||  
 QY 361 TTCCCTGGCTGTGACTTCATCGTTTGCACAACTGCAGTTCCTCGTGCAGTGTCAAAATCAT 420  
 |||||||  
 Db 530 ttccctggctgtacttcacgtttgccaactgcagttcctcgtgcagtgctcaaatcat 589  
 |||||||  
 QY 421 TCTGTGGACCTGACATTCAGCTCCTCATCAATTCCAAGATCAAAAAGCAGACGTTGGTA 480  
 |||||||  
 Db 590 tctgtgacctgacattgcagctcctcatcaattccaagatcaaaaagcagactgtgta 649  
 |||||||  
 QY 481 ACAGTGTGTGAGTCTGGAGTTCAGAGTAAGAACATCTACCAGAAATCTCTCAGTTTGTG 540  
 |||||||  
 Db 650 acagtgtgtgagctctggagttcagagtaagaacaatctaccagaatctctcagttttg 709  
 |||||||  
 QY 541 CTGCATTACTTACAGGTCAACTCTACCATATCAGTCAAGGTGGGATAATTTCCAGTATGTG 600  
 |||||||  
 Db 710 ctgcattacttacaggttcaactctaccatatacagtcagggggaagaaactgagtagtg 769  
 |||||||  
 QY 601 GATACAAACACTTTCCCTCTTGATAATGTGCTATCCGCTCTTCTATATAGTGTGACAG 660  
 |||||||  
 Db 770 gatataaacactttccctcttgataatgtgtctatccgtctcttctatatagtagctcagac 829  
 |||||||  
 QY 661 TGA 663  
 ||||  
 Db 830 tga 832

## RESULT 4

AAQ53537  
 ID AAQ53537 standard; cDNA; 720 BP.

XX AC AAQ53537;

XX DT 19-JUN-1994 (first entry)

XX DE Sequence of the coding region of a murine CD30-L cDNA clone





```
PT therapy
XX Claim 1; Figure 5a; 59pp; English.
PS
XX CD30-L is a ligand for CD30, the 120kd surface antigen widely used
CC as a clinical marker for Hodgkin's lymphoma and related haematologic
CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
CC L and other derived prods. can be used for elucidating the roles
CC that CD30 and CD30-L may play in the immune system and for diagnosis
CC and therapy. It can be isolated as follows. A cDNA library prep'd from
CC the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion
CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L.
CC This cDNA can then be used as a probe to screen a human PBL cDNA
CC library to obtain cDNA encoding human CD30-L.
XX
SQ Sequence 648 BP; 175 A; 166 C; 136 G; 171 T; 0 other;

Query Match 60.7%; Score 402.2; DB 14; Length 648;
Best Local Similarity 79.0%; Pred. No. 1.7e-117;
Matches 492; Conservative 0; Mismatches 128; Indels 3; Gaps 1;

QY 44 CGAGGCCCTGGAGAACACAAAGTCGAGCTACTTCTACCTCAGCACCACCGCACTGG--- 100
Db 26 ccagccacctgggaccacgagccgagctatttctatttgaccacagccactctgctc 85

QY 101 TGTGCTTGTGTGGCAGTGGCGATCATCTGTGTACTGTGTAGTCCAGAAAAGGACTCCA 160
Db 86 tgtgcttcttcacgtggccactattatggtgtgtgcttcagagggagcactcca 145

QY 161 CTCCAATACACTGAGAGGCCCTTAAAGGAGGAATTCCTCAGAGATCTCTCT 220
Db 146 ttcccaactcaactgacaactcctccctcaagaggagaaattgctcagaagacctctat 205

QY 221 GTACCTGAAAAGTACTCCATCCCAAGATCATGGGGCTACCTTCCAAAGTGTCAAGCATC 280
Db 206 gtaacctgaagagctcaattcaagaagtcagtgccctaccctccaaagtggcaagcattc 265

QY 281 TCACCAATACCAACTGTGATGATGAAGAGATGCGACCATCCAGGACTCATATACCAAG 340
Db 266 taacaaacaaagtgtgtcttggaacaaagatggcattctccatggagtcagatcag 325

QY 341 ACGGGAACTGATAGTCCCAATCCCTGGCTGTACTGTACTGTTCATCGTTGCAACTGCAGTCC 400
Db 326 atgggaatctgtgatacccaattccctgggtgttacttcaattgccaactgcagttc 385

QY 401 TGTGTCAGTGTCTCAATTCATCTGTGGACCTGACATTCGACGTCTCTCATCAATTCCAAGA 460
Db 386 tigtacaatgcccaataaattctgtcgatctgaagtggagcttctcatcaacaagcata 445

QY 461 TCAAAAGCAGAGGTGGTAACAGTGTGTGAGTGTGGAGTTCAGAGTAAGAACAATCTACC 520
Db 446 tcaaaaaaacagggccctggtgacagtggtgagctggaatgcaaacgaaacacagtatacc 505

QY 521 AGAATCTCTCTAGTTTTCCTGCATCTACTTACAGGTCACTCTACCATATCATGTCAGGG 580
Db 506 agaattctctcaattctgtgattacctgcaggttcaacaccacacatcatcagtcagt 565

QY 581 TGGATAATTTCCAGTATGTGGATACAAACACTTTCCTCTTGTGATAATGTGCTATCCGCT 640
Db 566 tggatatactcagttacacagatgatacagaagccacttctcttgagaatgtgtgtgctatct 625

QY 641 TCTTATATAGTACTCAGACTGA 663
Db 626 tcttatacagtaattcagactga 648

RESULT 6
AAQ53538
ID AAQ53538 standard; cDNA; 705 BP.
XX
AC AAQ53538;
XX
```

```
DT 19-JUN-1994 (first entry)
XX
DE Sequence of the coding region of a human CD30-L cDNA clone
DE encoding additional N-terminal amino acids.
XX
KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
KW CD30 ligand; CD30-L; TNF; NGF; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..705
FT /tag= a
XX
FN WO9324135-A.
XX
PD 09-DEC-1993.
XX
PF 25-MAY-1993; 93WO-US04926.
XX
PR 26-MAY-1992; 92US-0889717.
PR 02-JUN-1992; 92US-0892459.
PR 15-JUN-1992; 92US-0899660.
PR 01-JUL-1992; 92US-0907224.
PR 27-OCT-1992; 92US-0966775.
XX
PA (IMMV ) IMMUNEX CORP.
XX
PI Armitage RJ, Goodwin RG, Smith CA;
XX
DR WPI: 1993-405417/50.
DR P-PSDB: AAR45009.
XX
PT New cytokine, CD30-L, which binds CD30 - used for developing
PT prods. for diagnosis, detection, purifications, research and
PT therapy
XX
PS Claim 1; Figure 7a; 59pp; English.
XX
CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
CC as a clinical marker for Hodgkin's lymphoma and related haematologic
CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
CC L and other derived prods. can be used for elucidating the roles
CC that CD30 and CD30-L may play in the immune system and for diagnosis
CC and therapy. It can be isolated as follows. A cDNA library prep'd from
CC the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion
CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L
CC (AAQ53535). This cDNA can then be used as a probe to screen a human PBL
CC cDNA library to obtain cDNA encoding human CD30-L (AAQ53536). An
CC anchored PCR technique was employed to isolate CD30-L human and murine
CC clones containing an additional 19 N-terminal amino acid sequence
CC (AAQ53537, AAQ53538).
XX
SQ Sequence 705 BP; 190 A; 186 C; 152 G; 177 T; 0 other;

Query Match 60.7%; Score 402.2; DB 14; Length 705;
Best Local Similarity 79.0%; Pred. No. 1.7e-117;
Matches 492; Conservative 0; Mismatches 128; Indels 3; Gaps 1;

QY 44 CGAGGCCCTGGAGAACACAAAGTCGAGCTACTTCTACCTCAGCACCACCGCACTGG--- 100
Db 83 ccagccacctgggaccacgagccgagctatttctatttgaccacagccactctgctc 142

QY 101 TGTGCTTGTGTGGCAGTGGCGATCATCTGTGTACTGTGTAGTCCAGAAAAGGACTCCA 160
Db 143 tgtgcttgttctcacggtggccactattatggtgtgtgcttcagagggagcgactcca 202

QY 161 CTCCAATACAACTGAGAGGCCCTTAAAGGAGGAATTCCTCAGAGGATCTCTCT 220
Db 203 ttcccaactcaactgacaacgtcccccctcaaaaggaggaaaattgctcagaagacctctat 262

QY 221 GTACCTGAAAAGTACTCCATCCCAAGATCATGGGGCTACCTTCCAAAGTGTCAAGCATC 280
```

Db 263 gtaactgaaagagctccatcaagaagtcattgggctccactccaaagtgcgaagc 322  
Qy 281 TCAACAATACCAAACTGTCATGGAAGAGATGGCCACCATCCACGGAGTCTATACCAAG 340  
Db 323 taacaaacaaagtgcttggaaacaaagatggcattcccatggagtcagatcatcag 382  
Qy 341 ACGGGAACCTGATAGTCCCAATTCCTCGGCTGTGACTTCATCGTTTGCAACTGCAGTCC 400  
Db 383 atgggaatctggtgatcccaattccctgggttgtaactcatcattggccaactgcagttc 442  
Qy 401 TCGTCAGTGTCAAAATCAATTCGTGGAGCTGACATGTGACGCTCCCTCATCAATTCCAAGA 460  
Db 443 ttgtacaatgccecaataattctgtogactctgaagttggagcttctcatcaacaagcata 502  
Qy 461 TCAAAAAGCAGACGTGGTAACAGTGTGACGTCGTGGAGTTCAGAGTAAGAATCTAC 520  
Db 503 tcaaaaacagggccctggagcagtggtgagctggagctggaatgcaaaagaaacagatacc 562  
Qy 521 AGAATCTCTCTCAGTGTGTCATTAATTCAGGTCAACTCTACAGGTCAACTCTACATATCAGTCAAGG 580  
Db 563 agaactctctcaattcttggtgattactgcaggtcaacaccaccataatcagtaag 622  
Qy 581 TGGATAATTCAGATGTGGATACAAACACTTTCCTCTGTGATAATGTGCTATCCGCTCT 640  
Db 623 tggatacatccagtcacatagatacaagcacctttctctcttgagaatgtgtgtccatct 682  
Qy 641 TCTTATATAGTACGCTCAGACTGA 663  
Db 683 tcttatacagtaattcagactga 705

## RESULT 7

AAV39012

ID AAV39012 standard; DNÀ; 1906 BP.

XX AC AAV39012;

XX DT 23-SEP-1998 (first entry)

XX DE CD30 ligand gene used in the course of the invention.

XX Human; CD30 ligand; alteration; immunoreactivity; human cell;  
KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;  
KW autoimmune disorder; rheumatoid arthritis; vaccine; ss.  
XX Homo sapiens.

XX OS

XX PN W09826061-A2.

XX PD 18-JUN-1998.

XX PF 08-DEC-1997; 97WO-US22740.

XX PR 01-DEC-1997; 97US-0982272.

XX PR 09-DEC-1996; 96US-0032145.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Cantwell M, Kipps TJ, Sharma S;

XX DR WPI; 1998-348521/30.

XX Vectors containing accessory molecule ligand genes - used for  
PT altering immunoreactivity of cells, particularly for treatment of  
PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis  
XX  
PS Disclosure; Page 114; 167pp; English.  
XX  
CC The present sequence represents a CD30 ligand gene. The sequence is  
CC used to exemplify the method of the invention. The specification  
CC describes a method for altering the immunoreactivity of human cells  
CC which comprises introducing a gene encoding an accessory molecule

CC ligand (AML) into the cells so that the AML is expressed on the surface  
CC of the cells. Vectors containing the AML genes can be used in gene  
CC therapy for treating neoplasia or autoimmune disorders such as rheumatoid  
CC arthritis. They can also be used for vaccination to produce immunity  
CC against a virus cell, bacteria, protein, fungus or neoplasia.  
XX  
SQ Sequence 1906 BP; 559 A; 447 C; 438 G; 462 T; 0 other;

Query Match 60.7%; Score 402.2; DB 19; Length 1906;

Best Local Similarity 79.0%; Pred. No. 2.9e-117;

Matches 492; Conservative 0; Mismatches 128; Indels 3; Gaps 1;

Qy 44 CGAGGCCCTGAGAGACACAAAGTCGACGTACTTCTACTCTACGACACACCGCAGCTGG--- 100

Db 197 ccagccacctgggacacacgagccgagctatttctattgaccacacccactctggctc 256

Qy 101 TGTGCTTGTGTTGGCAGTGGCGATCATTTCTGTACTGTGTAGTCCAGAAAAGGACTCCA 160

Db 257 tgtgcttgtcttcacgggtggccactattatggtgtgtgttcagagggagcagactcca 316

Qy 161 CTCCAATATACAACTGAGAGAGGCCCCCTTAAAGGAGGAAATGCTCAGAGGATCTCTTCT 220

Db 317 ttcccaactcactgacacacgtccctccctcaagaggaggaattgtctcagaagacctcttat 376

Qy 221 GTACCCCTGAAAGTACTCCATCCAAGAGTCAATGGGCTTACTCTCAAGTGTCAAGAGCATC 280

Db 377 gtatccttgaaagaggtccattcaagaagtcattgggcccactcccaagtggcaagcactc 436

Qy 281 TCAACAATACCAAACTGTCTATGSAACGAAGATGCCACCATCCACGGACTATATACCAAG 340

Db 437 taacaaacccaagtgtcttggaacaaagatggcattctccatggagtcagatcatcagg 496

Qy 341 ACGGGAACCTGATAGTCCCAATTCCTCGGCTGTGACTTCATCGTTTGCCAACTGCAGTTC 400

Db 497 atgggaatctggtgatcccaattccctggtgtgtactcatcatttgccaactgcagtttc 556

Qy 401 TCGTCAGTGTCTCAAAATCATTTCTGTGGACCTGACATTTGCAGCTCTCTCATCAATTCCAAGA 460

Db 557 ttgtacaatgcccaataattctctgcatctgaaagtggagcttctctatcaacaagcata 616

Qy 461 TCAAAAAGCAGACGTGTGTGTAACAGTGTGTGAGTCTGGAGTTCAGAGTAAGAACAATCTACC 520

Db 617 tcaaaaacagggccctggtgacagtggtgagctggaatgcaaacgaaacacgataacc 676

Qy 521 AGAATCTCTCTCAGTGTGCTGCTGCTACTTACTTACAGGTCAACTCTACCATATCAGTCAGG 580

Db 677 agaactctctcaattctgtggtattacctgcaggtgcaacaccaccataatcagtcagt 736

Qy 581 TGGATAATTTCCAGTATGTGGATACAAACACTTTCCTCTTGTGATAATGCTGCTCCGCTCT 640

Db 737 tggatatactccagtcacatagatacaagaaccttctctcttgagaatgtgtgtccatct 796

Qy 641 TCTTATATAGTCTCAGACTGA 663

Db 797 tcttatacagtaattcagactga 819

## RESULT 8

AAF58252

ID AAF58252 standard; DNA; 936 BP.

XX AC AAF58252;

XX DT 24-APR-2001 (first entry)

XX DE Oligonucleotide D1835.

XX KW Electron-transfer group; ETM; mismatch; genotyping;

XX PR gene expression; ss.

XX OS Synthetic.

```
PN WO200107665-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-US20476.
XX
PR 26-JUL-1999; 99US-0145695.
XX
PR 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Umek RM;
XX
PD 01-FEB-2001.
XX
DR WPI; 2001-159728/16.
XX
XX Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface
XX
PS Example 6; Page 127; 159pp; English.
XX
XX The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
SQ Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;

Query Match 6.4%; Score 42.6; DB 22; Length 936;
Best Local Similarity 1.3%; Pred. No. 0.002;
Matches 6; Conservative 260; Mismatches 199; Indels 0; Gaps 0;

QY 188 TTAAGGAGGAATGCTCAGAGATCTCTCTGTACCCCTGAAAGTACTCCATCCAGA 247
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
40 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
248 AGTCATGGGCTACCTCAAGTGTCAAGCATCTCAACAATACCAAACTGTCATGGAAG 307
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
100 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
308 AAGATGCCACCTCCAGGACTCATATACAGGACGGGAACCTGATAGTCCAAATCCCTG 367
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
160 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
368 GCTGTACTTCACTGCTGTTGCCAACTGCAGTTCCTCTGTCAGTGTCAAAATCATTTCTGTGG 427
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
220 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
428 ACCTGACATTCAGCTCCTCATCAATTCAGATCAAAAGCAGACGTTGTAACAGTGT 487
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
280 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
488 GTGAGTCTGGAGTTCAGAGTAAGAACATCTACCAAGATCTCTCTCAGTCTTTTGTGCTGATT 547
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
340 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
548 ACTTACAGGTCAACTCTACCATATCAGTCAGGTGGATAATTTCCAGTATGTGGATACAA 607
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
400 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
608 AACTTTCCTCTGTGATAATGTGCTATCCGCTCTCTCTATATAGTA 652
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
460 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
AAF58252/c
ID AAF58252 standard; DNA; 936 BP.
XX
AC AAF58252;
```

```
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide D1835.
XX
KW Electron-transfer group; ETM; mismatch; genotyping;
KW gene expression; ss.
XX
OS Synthetic.
XX
PN WO200107665-A2.
XX
PD 01-FEB-2001.
XX
DR 26-JUL-2000; 2000WO-US20476.
XX
PR 26-JUL-1999; 99US-0145695.
XX
PR 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Umek RM;
XX
DR WPI; 2001-159728/16.
XX
XX Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface
XX
PS Example 6; Page 127; 159pp; English.
XX
XX The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
SQ Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;

Query Match 6.4%; Score 42.6; DB 22; Length 936;
Best Local Similarity 1.1%; Pred. No. 0.002;
Matches 6; Conservative 292; Mismatches 231; Indels 0; Gaps 0;

QY 124 ATCATTCCTGTTAGTCCAGAAAAGGACTCCACTCCAAATACAACTGAGAAGGCC 183
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
710 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
184 CCCCTTAAAGGAGGAATGCTCAGAGGATCTCTCTGTACCTGAAAGTACTCCATCC 243
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : :
650 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
244 AAGAAGTCATGGCCCTACCTCCAAAGTCAAAAGCATCTCAACAATACCAAACTGTGATGG 303
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : :
590 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
304 AACGAAGATGCGACCATCCAGGACTCATATACAGGACGGGAACCTGATAGTCAATTC 363
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : :
530 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
364 CTGCTTGTACTTCTCATCGTTTGCCCAACTGCAGTTCCTCGTGCAGTCTCAATCATCT 423
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : :
470 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
424 GTGACCTGACATTCGAGCTCTCATCAATTCCAAGATCAAAAGCAGACGTTGTGAACA 483
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : :
410 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
484 GTGTGTGAGTCTGGAGTTCAGAGTAAGAACATCTACCAAGATCTCTCAGTCTTTTGTG 543
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : :
350 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Query Match 6.4%; Score 42.6; DB 22; Length 936;
Best Local Similarity 1.1%; Pred. No. 0.002;
Matches 6; Conservative 292; Mismatches 231; Indels 0; Gaps 0;
```

D	b	220	www.....279
O	y	428	ACCTGACATTGCAGTCTCTCATCAATCCAAAGATCAAAAAGCAGACGCTTGTTGAACAGTGT
D	b	280	www.....
O	y	488	GTAGTCCTGGAGTTTCAGAGTAAGAACAATCTACCAGAAATCTCTCTCAGTTTTTTTGTGCGAATT
D	b	340	www.....399
O	y	548	ACTTACAGGTCAACTCACCATATACAGTCAGGCTGGATAATTTCCAGCATATGTGGATACAA
D	b	400	www.....
O	y	608	ACACTTTCCCCTCTTCGATAAATGCTATCCGCTCTTCTTATATAGTA
D	b	460	www.....504
 RESULT 11 AAF58254/c			
X	x	ID	AAF58254 standard; DNA; 936 BP.
X	x	AC	AAF58254;
X	x	DT	24-APR-2001 (first entry)
X	x	DE	Oligonucleotide D1875.
X	x	KW	Electron-transfer group; ETM; mismatch; genotyping;
X	x	KW	gene expression; ss.
X	x	OS	Synthetic.
X	x	PN	WO200107665-A2.
X	x	PD	01-FEB-2001.
X	x	PF	26-JUL-2000; 2000WO-US20476.
X	x	PR	26-JUL-1999; 99US-0145695.
X	x	PR	17-MAR-2000; 2000US-0190259.
X	x	PA	(CLIN-) CLINICAL MICRO SENSORS INC.
X	x	PI	Umek RM;
X	x	DR	WPI; 2001-159738/16.
P	T	Nucleic acids containing electron-transfer group, useful as labels in	
P	T	hybridization assays, e.g. for genotyping, allowing repeat analyses on	
P	T	a single surface -	
X	x	Example 6; Page 127; 159pp; English.	
C	C	The present invention relates to a composition comprising two nucleic	
C	C	acids each containing an electron-transfer group (ETM) having	
C	C	different redox potentials. The invention is used for electronic	
C	C	detection of nucleic acids, especially of substitutions (mismatches)	
C	C	and single-nucleotide polymorphisms, e.g. for genotyping,	
C	C	monitoring gene expression.	
X	x	Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;	
 Query Match 6.4%; Score 42.6; DB 22; Length 936; Best Local Similarity 1.1%; Pred. No. 0.002; Matches 6; Conservative 292; Mismatches 231; Indels 0; Gaps			
O	y	124	ATCATCTGCTAGTGGTAGTCCAGAAAAAGGACTCCCAATCAACTGAGAAGGCC
D	b	710	www.....651







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OM nucleic - nucleic search, using sw model

Run on: September 5, 2001, 21:50:21 ; Search time 1465.36 Seconds  
(without alignments)  
6998.361 Million cell updates/sec

Title: US-09-628-126-18

Perfect score: 663

Sequence: 1 ATCGAGTGTGAGCCCGGCTC.....TATATAGTACTCAGACTGA 663

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba1.\*

2: gb\_ba2.\*

3: gb\_ba3.\*

4: gb\_in1.\*

5: gb\_in2.\*

6: gb\_in3.\*

7: gb\_om.\*

8: gb\_ov.\*

9: gb\_pat1.\*

10: gb\_pat2.\*

11: gb\_ph.\*

12: gb\_pl1.\*

13: gb\_pl2.\*

14: gb\_pl3.\*

15: gb\_pl4.\*

16: em\_ba1.\*

17: em\_ba2.\*

18: em\_fun.\*

19: em\_htgo\_hum.\*

20: em\_htgo\_inv.\*

21: em\_htgo\_rod.\*

22: em\_htg\_hum1.\*

23: em\_htg\_hum2.\*

24: em\_htg\_hum3.\*

25: em\_htg\_hum4.\*

26: em\_htg\_hum5.\*

27: em\_htg\_hum6.\*

28: em\_htg\_hum7.\*

29: em\_htg\_hum8.\*

30: em\_htg\_inv1.\*

31: em\_htg\_inv2.\*

32: em\_htg\_other.\*

33: em\_htg\_rod.\*

34: em\_hum1.\*

35: em\_hum2.\*

36: em\_hum3.\*

37: em\_hum4.\*

38: em\_hum5.\*

39: em\_hum6.\*

40: em\_hum7.\*

41: em\_in.\*

42: em\_om.\*

43: em\_or.\*

44: em\_ov.\*  
45: em\_pat.\*  
46: em\_ph.\*  
47: em\_pl.\*  
48: em\_ro.\*  
49: em\_sts.\*  
50: em\_sy.\*  
51: em\_un.\*  
52: em\_vi.\*  
53: gb\_sts1.\*  
54: gb\_sts2.\*  
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91: gb\_vil2.\*  
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98: em\_ba3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	663	100.0	663	9	AR007977	AR007977 Sequence
2	663	100.0	663	10	IL6911	IL6911 Sequence 18
3	663	100.0	663	10	I69504	I69504 Sequence 18
4	663	100.0	720	9	AR007968	AR007968 Sequence
5	663	100.0	720	10	IL6902	IL6902 Sequence 5
6	663	100.0	720	10	I69495	I69495 Sequence 5
7	663	100.0	1783	94	MUSCD30	L09754 Mus musculu
8	402.2	60.7	648	9	AR007978	AR007978 Sequence



## ALIGNMENTS

	Query Match	100.0%	Score 663;	DB 9;	Length 663;
	Best Local Similarity	100.0%;	Pred. NO. 8.le-189;		
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Db	1	ATGCAGGTGCAGCCCGGCTCGGTAGCCAGGCCCTGGAGAACACAGAGCCCTGGAGAAGC	60		
QY	61	ACAAGTCGCAAGCTACTTCTACCTCAGCACACACCGCACTGGTGTGCCTTGTGTGTGCAGTG	120		

Qy	61	ACAAGTCGACGTA	CTTCTACCTCAGCACACCGCACTGGTGCCCTGTTGTGGCAGTG	120
Db	61	ACAAGTCGACGTA	CTTCTACCTCAGCACACCGCACTGGTGCCCTGTTGTGGCAGTG	120
Qy	121	CGGATCA	TTCTGGTACTGTCAGAGAAAGACATCCCACTCCAAATACAACTGAGAAG	180
Db	121	CGGATCA	TTCTGGTACTGTCAGAGAAAGACATCCCACTCCAAATACAACTGAGAAG	180
Qy	181	GGCCCCCTTAAAGGAGGAAAT	TGCTCAGAGGATCTCTTCTACCCCTGAAAGTACTCCCA	240
Db	181	GGCCCCCTTAAAGGAGGAAAT	TGCTCAGAGGATCTCTTCTACCCCTGAAAGTACTCCCA	240
Qy	241	TCCAGAAAGTCATGGGCC	TACTCTCCAAAGTGTCAAAGCATCTCAACAAATACCAACTGTCA	300
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Qy	301	TGGAACGAAGATGGAC	CACTCCACGGACTCATATACAGGACGGGAACCTGATAGTCCAA	360
Db	301	TGGAACGAAGATGGAC	CACTCCACGGACTCATATACAGGACGGGAACCTGATAGTCCAA	360
Qy	361	TTCCCTGGCTGTACT	TCATCGTTTGCCCACTGCAGTTCCCTCGTGCACTGCTCAATCAT	420
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Qy	421	TCTGTGGACCTGCAT	CTTCAGTTCATCAATTTCCAAAGATCAAAAAGCAGACGTTGGTA	480
Db	421	TCTGTGGACCTGCAT	CTTCAGTTCATCAATTTCCAAAGATCAAAAAGCAGACGTTGGTA	480
Qy	481	ACAGTGTGTGAGTCTGGAG	TTTCAGAGTAAGAACAATCTACCAAGATCTCTCTCAGTTTTTG	540
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Qy	541	CTGCATTA	TACTTACAGGTCAACTCTACCATATCAGTCAGGGTGGATAATTTCCAGTATGTG	600
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Qy	601	GATACAAACACTTTCCCT	CTTGATAATGTGCTATCCGCTCTCTTATATAGTAGCTCAGAC	660
Db	601	GATACAAACACTTTCCCT	CTTGATAATGTGCTATCCGCTCTCTTATATAGTAGCTCAGAC	660
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Db	661	TGA	663	
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DEFINITION	Sequence 5 from patent US 5753203.			
ACCESSION	AR007968			
VERSION	AR007968.1 GI:3967077			
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 720)			
AUTHORS	Goodwin, R.G., Smith, C.A., Armitage, R.J. and Gruss, H.			
TITLE	CD30 ligand conjugates			
JOURNAL	Patent: US 5753203-A 5 19-MAY-1998;			
FEATURES	Location/Qualifiers			
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ORIGIN	/organism="unknown"			

Query Match	100.0%	Score 663;	DB 9;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 8.2e-189;		
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Query Match	100.0%	Score 663;	DB 10;	Length 720;
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Query Match	100.0%	Score 663;	DB 10;	Length 720;
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Qy 61 ACAAGTCGACAGTACTTCTACCTCAGCACCACCGCAGTGGTGGCTTGTGTGGCAGTG 120
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Qy 421 TCTGTGGACCTGACATTTGACGCTTCTCATCAATTCCAAGATCAAAAGCAGAGCTTGGTA 480
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Db 658 GATACAAACACTTTCCTCTTGATATGTGCTATCGCTCTCTTATATAGTACGTACAG 717
Qy 661 TGA 663
Db 718 TGA 720

RESULT 7
MUSCD30 1783 bp mRNA ROD 23-AUG-1995
LOCUS Mus musculus Cd30 ligand mRNA, complete cds.
DEFINITION L09754
ACCESSION L09754
VERSION L09754.1 GI:349288
KEYWORDS CD30 ligand; transmembrane protein type II.
SOURCE Mus musculus cdna to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1783)
AUTHORS Smith,C.A., Gruss,H.J., Davis,T., Anderson,D., Farrah,T., Baker,E.,
Sutherland,G.R., Brannan,C.I., Copeland,N.G., Jenkins,N.A.,
Grabstein,K.H., Gliniak,B., McAllister,I.B., Fanslow,W.,
Alderson,M., Falk,B., Gimpel,S., Gillis,S., Din,W.S., Goodwin, R.G.
and Armitage,R.J.
CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
ligand defines an emerging family of cytokines with homology to TNF
Cell 73 (7), 1349-1360 (1993)
FEATURES
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/db_xref="taxon:10090"
source
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/cell_type="r-cell"
113..832
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/product="CD30 antigen"
/protein_id="AA74595.1"
/db_xref="GI:349288"
/translation="MEPGLQAGSCGAPSDPAMQVQPSVAPRSTREWRSTSRYS
FYLSSTALVCLVVAAILLVVQKDKSTNTTEKAPLKGNGSDFLTKLSTPSKK
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VDLTQLLINSKIKKOTLVTVYCESGVQSKNIYQNLQFLHLHYQVNSTISVRVDFQY
VDNTPTFDNLVSLVFLYSSSD"
BASE COUNT 515 a 411 c 407 g 450 t
ORIGIN
Query Match 100.0%; Score 663; DB 94; Length 1783;
Best Local Similarity 100.0%; Pred. No. 9.2e-189;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCAGGTGCACGCCGGCTCGTAGCCAGCCCTGGAGAGACAGAGGCCCTGGAGAGC 60
Db 170 ATGCAGGTGCACGCCGGCTCGTAGCCAGCCCTGGAGAGACAGAGGCCCTGGAGAGC 229
Qy 61 ACAAGTCGACGACTACTTCTACCTCAGCACCACCGCAGTGGTGGCTTGTGTGGCAGTG 120
Db 230 ACAAGTCGACGACTACTTCTACCTCAGCACCACCGCAGTGGTGGCTTGTGTGGCAGTG 289
Qy 121 GCGATCATCTCGTACTGTTAGTCCAGAAAAGGACTCCACTCCAATACAACTGAGAGAG 180
Db 290 GCGATCATCTCGTACTGTTAGTCCAGAAAAGGACTCCACTCCAATACAACTGAGAGAG 349
Qy 181 GCCCCCTTAAAGGAGGAATTTGCTCAGAGATCTCTTCTGTACCTGAAAAGTACTCCA 240
Db 350 GCCCCCTTAAAGGAGGAATTTGCTCAGAGATCTCTTCTGTACCTGAAAAGTACTCCA 409
Qy 241 TCCAAAGAGTCATGGCCCTACCTCCAAGTGTCAAAAGCATCTCAACAATACCAACTGTCA 300
Db 410 TCCAAAGAGTCATGGCCCTACCTCCAAGTGTCAAAAGCATCTCAACAATACCAACTGTCA 469
Qy 301 TGGAAACGAAGATGGACACATCCAGGACTCATATACAGGAGCGGGAACCTGATAGTCCA 360
Db 470 TGGAAACGAAGATGGACACATCCAGGACTCATATACAGGAGCGGGAACCTGATAGTCCA 529
Qy 361 TTCCTCGCTTGTACTTTCATCGTTTGGCAACTGCAGTTTCCCTCGTGCAGTGTCAAAATCAT 420
Db 530 TTCCTCGCTTGTACTTTCATCGTTTGGCAACTGCAGTTTCCCTCGTGCAGTGTCAAAATCAT 589
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AR007978
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LOCUS AR007978 648 bp DNA PAT 04-DEC-1998  
DEFINITION Sequence 22 from patent US 5753203.  
ACCESSION AR007978  
VERSION AR007978.1 GI:3967087  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 648)  
AUTHORS Goodwin,R.G., Smith,C.A., Armitage,R.J. and Gruss,H.  
TITLE CD30 ligand conjugates  
JOURNAL Patent: US 5753203-A 22 19-MAY-1998;  
FEATURES Location/Qualifiers  
source 1..648  
BASE COUNT 175 a 166 c 136 g 171 t  
ORIGIN

Query Match 60.7%; Score 402.2; DB 9; Length 648;  
Best Local Similarity 79.0%; Pred. No. 3.5e-110;  
Matches 492; Conservative 0; Mismatches 128; Indels 3; Gaps 1;

QY 44 CGAGGCCCTGGAGAGCACAAGTCGAGCTACTTCTACCTCAGCACCCGCACTGG--- 100  
DB 26 CCAGCCACCTGGGACCAAGCCGAGCTATTCTATTGACCAAGCCGCACTCTGGCTC 85  
QY 101 TGTGCTTGTGTGGCAGTGGGATCATCTGTGCTAGTCCAGAAAAGGACTCCA 160  
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QY 221 GTACCCCTGAAAGTACTCCATCCAAAGAGTATGGGCTTACCTCCAAAGTGTCAAAGCATC 280  
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QY 281 TCACAAATACCAAACTGTGTAACAGAGATGGCACTCCACGACTCATATACCAGG 340  
DB 266 TAAACAAACCAAGTGTCTTGGAAACAAGATGGCACTTCTCCATGGAGTCAGATATCAGG 325  
QY 341 ACGGGAACCTGATAGTCCAAATTCCTGGCTGTACTTCATCTGTTGCCAACTGCAGTTCC 400  
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QY 401 TCGTGCAGTGTCAAAATCATTTCTGTGGACCTGACATTCGAGCTCCTCATCAATTTCCAAGA 460  
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QY 461 TCAAAAAGCAGACGTTGTAACAGTGTGTGAGTCTGGAGTTCAGAGTAGAAGACATCTACC 520  
DB 446 TCAAAAACAGCCCTGGTGACAGTGTGTGAGTCTGGAAATGCAACGAAACAGTATACC 505  
QY 521 AGAATCTCTCAGTTTTTGTGCTGAATTAATCTACAGTCAACTCTACCATATCAGTCAGGG 580  
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QY 641 TCTTATATAGTACGACTGA 663  
DB 626 TCTTATACAGTAATTCAGACTGA 648

RESULT 9  
LOCUS I16912  
DEFINITION Sequence 22 from patent US 5480981.  
ACCESSION I16912

VERSION I16912.1 GI:1251820  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 648)  
AUTHORS Goodwin,R.G., Smith,C.A., Armitage,R.J. and Gruss,H.  
TITLE CD30 ligand  
JOURNAL Patent: US 5480981-A 22 02-JAN-1996;  
FEATURES Location/Qualifiers  
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BASE COUNT 175 a 166 c 136 g 171 t  
ORIGIN

Query Match 60.7%; Score 402.2; DB 10; Length 648;  
Best Local Similarity 79.0%; Pred. No. 3.5e-110;  
Matches 492; Conservative 0; Mismatches 128; Indels 3; Gaps 1;

QY 44 CGAGGCCCTGGAGAGCACAAGTCGAGCTACTTCTACCTCAGCACCCGCACTGG--- 100  
DB 26 CCAGCCACCTGGGACCAAGCCGAGCTATTCTATTGACCAAGCCGCACTCTGGCTC 85  
QY 101 TGTGCTTGTGTGGCAGTGGGATCATCTGTGCTAGTCCAGAAAAGGACTCCA 160  
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RESULT 10  
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DEFINITION Sequence 22 from patent US 5677430.  
ACCESSION I69505  
VERSION I69505.1 GI:2831627  
KEYWORDS Unknown.  
SOURCE

ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 648)  
AUTHORS Goodwin,R.G., Smith,C.A., Armitage,R.J. and Gruss,H.  
TITLE Antibodies directed against CD30 ligand  
JOURNAL Patent: US 5677430-A 22 14-OCT-1997;  
FEATURES Location/Qualifiers  
source 1..648  
BASE COUNT 175 a 166 c 136 g 171 t  
ORIGIN

Query Match 60.7%; Score 402.2; DB 10; Length 648;  
Best Local Similarity 79.0%; Pred. No. 3.5e-110;  
Matches 492; Conservative 0; Mismatches 128; Indels 3; Gaps 1;

QY 44 CGAGCCCTGGAGAGCACAAGTCGACGACTTCTTACCTCAGCACCACCGCAGCTGG--- 100  
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RESULT 11  
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DEFINITION Sequence 7 from patent US 5753203.  
ACCESSION AR007969  
VERSION AR007969.1 GI:3967078  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 705)  
Unclassified.  
AUTHORS Goodwin,R.G., Smith,C.A., Armitage,R.J. and Gruss,H.  
TITLE CD30 ligand  
JOURNAL Patent: US 5480981-A 7 02-JAN-1996;

AUTHORS Goodwin,R.G., Smith,C.A., Armitage,R.J. and Gruss,H.  
TITLE CD30 ligand conjugates  
JOURNAL Patent: US 5753203-A 7 19-MAY-1998;  
FEATURES Location/Qualifiers  
source 1..705  
BASE COUNT 190 a 186 c 152 g 177 t  
ORIGIN

Query Match 60.7%; Score 402.2; DB 9; Length 705;  
Best Local Similarity 79.0%; Pred. No. 3.5e-110;  
Matches 492; Conservative 0; Mismatches 128; Indels 3; Gaps 1;

QY 44 CGAGCCCTGGAGAGCACAAGTCGACGACTTCTTACCTCAGCACCACCGCAGCTGG--- 100  
Db 83 CGAGCCACTGGGACACAGAGCCGAGCTATTCTATTGGACCACAGCCACTCTGGCTC 142  
QY 101 TGTGCTTTGTTGTGCGAGTGGCGATCATTTCTGGTACTGGTAGTCCAGAAAAGGACTCCA 160  
Db 143 TGTGCTTTGTTGTGCGAGTGGCGATCATTTCTGGTACTGGTAGTCCAGAAAAGGACTCCA 202  
QY 161 CTCCAAATACAACTGAGAGGCCCCCTTAAAGAGGAGAAATGCTCAGAGGACTCTCTTCT 220  
Db 203 TTCCCAACTCAGTACAACTGAGAGGCCCCCTTAAAGAGGAGAAATGCTCAGAGGACTCTCTTAT 262  
QY 221 GTACCTGAAAGTACTCCATCCAAAGAGTCAATGGCCCTACCTCCCAAGTGTCAAGCAATC 280  
Db 263 GTATCTGAAAGAGTCTCATCAAGAGTCAATGGCCCTACCTCCCAAGTGTCAAGCAATC 322  
QY 281 TCACAAATACCAAACTGTCATGGAACGAGATGGCACCACCTCAGGACTCATATACAGG 340  
Db 323 TAAACAAACCAAGTTGCTTGGACAAAGATGGCATTTCCATGGAGTCAGATATACAGG 382  
QY 341 ACGGAACCTGATAGTCCAAATCCCTGGGTTGTACTTCATCGTTTGGCAACTCAGTTCC 400  
Db 383 ATGGGAATCTGGTATCCAAATCCCTGGGTTGTACTTCATCGTTTGGCAACTCAGTTTC 442  
QY 401 TCGTGCAGTGTCAATCATCTGTGGACCTGACATTCAGCTCAGCTCCATCAATTCACAAG 460  
Db 443 TTGTACAATGCCAAATTAATCTGTGATCTGAAGTTGGAGCTTCATCAACAAGCATA 502  
QY 461 TCAAAAGCAGACGTTGGTAACAGTGTGTGAGTCTGGAGTTCAGAGTAAGAACATCTACC 520  
Db 503 TCAAAAGCAGCCCTGGTGACAGTGTGTGAGTCTGGAGTTCAGAGTAAGAACATCTACC 562  
QY 521 AGAATCTCTCAGTTTGTGTCATTAATACAGTCAACTCTACCATATCATCATCAGG 580  
Db 563 AGAATCTCTCAATCTTGTGTTGATTAATACAGTCAACTCTACCATATCATCATCAG 622  
QY 581 TGGATAATTTCCAGTATGGGATACAAACACTTTCCCTCTTGATATATGCTATCCGTC 640  
Db 623 TGGATACATTCAGTATACAGTATACAAACACTTTCCCTCTTGATATATGCTATCCGTC 682  
QY 641 TCTTATATAGTAGTCAGACTGA 663  
Db 683 TCTTATACAGTAATTCAGACTGA 705

RESULT 12  
LOCUS 116903 705 bp DNA PAT 03-APR-1996  
DEFINITION Sequence 7 from patent US 5480981.  
ACCESSION 116903  
VERSION 116903.1 GI:1251811  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 705)  
Unclassified.  
AUTHORS Goodwin,R.G., Smith,C.A., Armitage,R.J. and Gruss,H.  
TITLE CD30 ligand  
JOURNAL Patent: US 5480981-A 7 02-JAN-1996;

FEATURES		Location/Qualifiers		BASE COUNT		ORIGIN	
source		1. .705		190 a		186 c 152 g 177 t	
ORIGIN		/organism="unknown"					
Query Match		60.7%; Score 402.2; DB 10; Length 705;					
Best Local Similarity		79.0%; Pred. No. 3.5e-110;					
Matches 492; Conservative		0; Mismatches 128; Indels 3; Gaps 1;					
Qy	44	CGAGGCCCTGGAGAACACAAAGTCCGAGCTACTTCTACCTCAGCACCACCGCACTGG---	100				
Db	83	CGAGCCACCTGGGACCAACGAGCCGAGCTATTTCTATTGACCAACGCACTCTGGCTC	142				
Qy	101	TGTGCTTTGTTGTGCGAGTGGGATCATCTGGTACTGGTACTGTCAGAGAAAGGACTCCA	160				
Db	143	TGTGCTTTGTTGTGCGAGTGGGATCATCTGGTACTGGTACTGTCAGAGAAAGGACTCCA	202				
Qy	161	CTCCAAATACAACTGAGAGAGGCCCCCTTAAAGAGAGAAATTTGTCAGAGATCTCTTCT	220				
Db	203	TTCCCAACTCACCTGACCAAGTCCCTTCAAGAGAGTCAATGAGGAGGAAATTTGTCAGAGACCTCTTAT	262				
Qy	221	GTACCCCTGAAAGTACTCCATCCAGAGAGTCAATGAGGAGGAAATTTGTCAGAGATCTCTTCT	280				
Db	263	TTCCCAACTCACCTGACCAAGTCCCTTCAAGAGAGTCAATGAGGAGGAAATTTGTCAGAGACCTCTTAT	322				
Qy	281	TCAACAAATACCAACTGTCATGGAACGAAGATGGCAACATCCACGGACTCATATACCAAG	340				
Db	323	TAAACAAACCAAGTGTCTTTGGAACAAAGATGGCAATTTCCATGGAGTCAGATATCAGG	382				
Qy	341	ACGGGAACCTGATAGTCCAAATTCCTCGCTTGTACTTCTATCGTTGCCAACTGCCGTTCC	400				
Db	383	ATGGGAATCTGGTGATCCAAATTCCTCGCTTGTACTTCTATCGTTGCCAACTGCCGTTCC	442				
Qy	401	TCGTGAGTGTCAAAATCATTTCTGTGACCTGCACATTCGAGCTCTCATCAATTTCCAAGA	460				
Db	443	TTGTACAAATGCCAAATAATTTCTGCGATCTGAAGTTGGAGCTTCTCATCAACAGCAT	502				
Qy	461	TCAAAAGCAGAGCTTGGTAAACAGTGTGTGAGTGTGAGTTCAGAGTGAAGAACATCTACC	520				
Db	503	TCAAAAGCAGAGCTTGGTAAACAGTGTGTGAGTGTGAGTTCAGAGTGAAGAACATCTACC	562				
Qy	521	AGAACTCTCTCAGTTTTCCTGCTGATTTCTTACAGTCAAACTCTACCATATCAGTCAGG	580				
Db	563	AGAACTCTCTCAGTTTTCCTGCTGATTTCTTACAGTCAAACTCTACCATATCAGTCAGG	622				
Qy	581	TGGATAATTTCCAGTATGTGGATCAAAACACTTTCCCTCTTGTGATATGTGCTATCCGCT	640				
Db	623	TGGATAATTTCCAGTATGTGGATCAAAACACTTTCCCTCTTGTGATATGTGCTATCCGCT	682				
Qy	641	TCCTATATAGTACGTCAGACTGA 663					
Db	683	TCCTATACAGTAATTCAGACTGA 705					
RESULT 13		HUMCD30		1906 bp		mRNA	
LOCUS		Homo sapiens		CD30 ligand		complete cds.	
DEFINITION		L09753		L09753.1		GI:349277	
ACCESSION		L09753		CD30 ligand; transmembrane protein type II.		SOURCE	
VERSION		1		Homo sapiens		cdna to mRNA.	
KEYWORDS		Homo sapiens		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
SOURCE		Unknown.		1 (bases 1 to 1906)		REFERENCE	
ORGANISM		Unclassified.		AUTHORS		Smith, C.A., Gruss, H.J., Davis, T., Anderson, D., Farrar, T., Baker, E.,	
REFERENCE		1 (bases 1 to 705)		TITILE		Antibodies directed against CD30 ligand	
AUTHORS		Goodwin, R.G., Smith, C.A., Armitage, R.J. and Gruss, H.		JOURNAL		Cell 73 (7), 1349-1360 (1993)	
TITLE		CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose		FEATURES		source	
JOURNAL		Cell 73 (7), 1349-1360 (1993)		Location/Qualifiers		/organism="unknown"	
				1. .705			







QY 510 GAACATCTACCAAGATCTCTCTCAGTTTTTGTGCAATTACTTACAGGTCAACTCTTACCAT 569  
 Db 438 ACACGTATACCAAGATCTCTCTCAATTCTTGTGGATTACCTGCAGSTCAACACCAACCAT 497  
 QY 570 ATCAGTCAGGGTGGATAATTTCCAGTATGTGGATACAAACACTTTCCCTCTTGATTAATGT 629  
 Db 498 ATCAGTCAATGTGGATACATTCCAGTACATAGATACAGCACCTTTCTCTTGAGAATGT 557  
 QY 630 GCTATCCGCTCTTCTTATATAGTAGCTCAGAC 660  
 Db 558 GTTGCCATCTCTTATACAGTAATTCAGAC 588

Search completed: September 6, 2001, 00:39:31  
 Job time: 10150 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2001, 10:29:26 ; Search time 50.89 Seconds  
(without alignments)  
571.961 Million cell updates/sec

Title: US-09-628-126-19  
Perfect score: 1141  
Sequence: 1 MQVPGSVASPWSTRPWS.....DTNTFPLDNLVSLYSSSD 220

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_16.\*

- 1: sp.archaea.\*
- 2: sp.bacteria.\*
- 3: sp.fungi.\*
- 4: sp.human.\*
- 5: sp.invertebrate.\*
- 6: sp.mammal.\*
- 7: sp.mhc.\*
- 8: sp.organelle.\*
- 9: sp.phage.\*
- 10: sp.plant.\*
- 11: sp.rodent.\*
- 12: sp.unclassified.\*
- 13: sp.vertebrate.\*
- 14: sp.virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	794.5	69.6	234	4	O43404 homo sapien
2	89.5	7.8	225	13	Q9IB42
3	89.5	7.8	401	2	P72902 synchocyst
4	89.5	7.8	847	14	Q9WIS1 human immun
5	89	7.8	169	11	Q9WV90 marmota mon
6	88	7.7	234	6	Q28320 capra hircu
7	87	7.6	896	10	Q9M9B0 arabidopsis
8	87	7.6	2013	5	Q96216 plasmodium
9	86.5	7.6	2195	3	Q02822 saccharomyc
10	86	7.5	280	6	Q9MYL6 macaca neme
11	86	7.5	674	3	Q06629 saccharomyc
12	85	7.4	699	14	Q9DP26
13	84.5	7.4	208	2	O68241
14	84.5	7.4	217	11	Q9ERG6
15	84.5	7.4	884	10	O81069
16	84	7.4	1110	10	Q9SDA5
17	82	7.2	282	14	Q9IC83
18	81.5	7.1	151	5	Q9GP20 globodera r
19	81.5	7.1	304	5	Q94382 caenorhabdi

20	81.5	7.1	304	5	Q94383	Q94383 caenorhabdi
21	81	7.1	866	10	Q9SUN4	Q9suna4 arabidopsis
22	81	7.1	1391	14	Q9DPR7	Q9dpr7 meleagrid h
23	81	7.1	1409	14	Q9ELH3	Q9elh3 meleagrid h
24	80.5	7.1	344	10	O81781	O81781 arabidopsis
25	80	7.0	165	1	Q58685	Q58685 methanococc
26	80	7.0	232	4	Q9UIV3	Q9uiv3 homo sapien
27	80	7.0	358	14	Q71050	Q71050 human immun
28	80	7.0	369	2	Q59532	Q55952 synchocyst
29	80	7.0	400	14	O11578	O11578 human immun
30	80	7.0	403	14	O11580	O11580 human immun
31	79.5	7.0	399	14	O11584	O11584 human immun
32	79.5	7.0	889	10	Q9SNA3	Q9sna3 arabidopsis
33	79	6.9	350	4	Q9NSP7	Q9nsp7 homo sapien
34	79	6.9	364	4	Q9HB11	Q9hbi1 homo sapien
35	79	6.9	366	2	Q9REN2	Q9ren2 buchnera ap
36	79	6.9	402	14	O11576	O11576 human immun
37	79	6.9	412	14	O11565	O11565 human immun
38	79	6.9	902	14	Q9DHL2	Q9dhl2 yaba-like d
39	78.5	6.9	234	6	Q9TJ3	Q9ttj3 equus cabal
40	78.5	6.9	1150	3	Q02511	Q02511 saccharomyc
41	78.5	6.9	1477	3	O74218	O74218 candida alb
42	78	6.8	427	3	Q94386	Q94386 schizosacch
43	78	6.8	616	5	O16770	O16770 caenorhabdi
44	77.5	6.8	539	14	P88843	P88843 avian infec
45	77.5	6.8	912	10	Q9FN96	Q9fn96 arabidopsis

ALIGNMENTS

RESULT 1  
O43404 ID O43404 PRELIMINARY; PRT; 234 AA.  
AC O43404;  
DT 01-JUN-1998 (TREMBLrel. 06, Created)  
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE CD30L PROTEIN.  
GN CD30L.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98007874; PubMed=9349718;  
RA Croager E.J., Abraham L.J.;  
RT "Characterisation of the human CD30 ligand gene structure.";  
RL Biochim. Biophys. Acta 1353:231-235(1997).  
DR EMBL; AF006384; AAB97877.1; -;  
DR EMBL; AF006381; AAB97877.1; JOINED.  
DR EMBL; AF006382; AAB97877.1; JOINED.  
DR EMBL; AF006383; AAB97877.1; JOINED.  
DR InterPro; IPR000478; -;  
DR InterPro; IPR003638; -;  
DR Pfam; PF00229; TNF; 1.  
DR ProDom; PD023087; -; 1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
DR SMART; SM00207; TNF; 1.  
SQ SEQUENCE 234 AA; 25963 MW; 37BA5733C7911751 CRC64;

Query Match 69.6%; Score 794.5; DB 4; Length 234;  
Best Local Similarity 69.2%; Pred. No. 8.1e-69;  
Matches 153; Conservative 26; Mismatches 35; Indels 7; Gaps 2;  
QY 1 MQVPGSVASPWSTRPWSRSFYLSLTAL-VCLVAVAILLVVQKRDSPNTE 59  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 20 MHVPAGSVAS-----HLGTTSRSYFYLTATLALCLVFTVATIMLVVQRTSDIPNSPD 73  
QY 60 KAPLKGNCSEDLFTCTLKSTPSKKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIV 119

```
Db 74 NVPLKGGNCSEDLCLILKRAPFKSWAYLQVAKHLNKTLSNWKDGLHGVRYQDGNLVI 133
Oy 120 QPGLYFYICQLQFLVQCSNHSVDLTQLLINSKIKQTLVTVCESGVSKNYIYNLSQF 179
Db 134 QPGLYFYICQLQFLVQCPNNSVDLKLXELLINKHKQXLVTVCSGMQTKHYIYNLSQF 193
Oy 180 LLHYLQVNSTISVRVDNFQYVDNTFPDLNVLVFLYSSD 220
Db 194 LLDYLVQVNTISVVDNTQYIDTSTFPLENVLISFLXNSD 234

RESULT 2
Q91B42 ID Q91B42 PRELIMINARY; PRT; 225 AA.
AC Q91B42;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TUMOR NECROSIS FACTOR.
OS Paralicthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Bothidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RA Hirano I., Nam B., Kurobe T., Aoki T.;
RT "Molecular cloning, characterization and expression of tumor necrosis
RT factor (TNF) cDNA and gene from Japanese flounder Paralicthys
RT olivaceus.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB040448; BAA94969.1; -
DR InterPro: IPR000478; -
DR Pfam: PF00229; TNF; 1.
DR PRINTS: PR01234; TNCRSISFCT.
DR PROSITE: PS50049; TNF.2; 1.
SQ SEQUENCE 225 AA; 24965 MW; 8F947FB25FC82658 CRC64;

Query Match 7.8%; Score 89.5; DB 13; Length 225;
Best Local Similarity 25.4%; Pred. No. 0.58;
Matches 31; Conservative 23; Mismatches 57; Indels 11; Gaps 5;

Oy 33 LVCLVAVAILVLVQKDSPTNTTERKAPLKGNCSE--DLFCLIKSTPSK-KSWAYL- 88
Db 10 IVALCLGVLAFSWYTNKSEMTOSGOTAAALSQKDKAEKTEPHNTLRQISSRAKAIHLE 69
Oy 89 ---QVSKHLNNTKLSW-NEDG---TIHGLYQDGNLIVQFGLYFIVCOLOFLVQCSNHS 141
Db 70 GRDEDETSENKLVWKNDEGLAFTQGGFELVDNHIIPRSLGYFYVQASFRVSCSD 129
Oy 142 VD 143
Db 130 AD 131

RESULT 3
P72902 ID P72902 PRELIMINARY; PRT; 401 AA.
AC P72902;
DT 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE HYPOTHETICAL 46.0 KDA PROTEIN.
GN SLR1066.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-97061201; PubMed-8905231;
MEDLINE-97061201; PubMed-8905231;
```

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RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Suglura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL: D90901; BAA16918.1; -
DR InterPro: IPR001296; -
DR Pfam: PF00534; Glycos_transf_1; 1.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 401 AA; 45951 MW; 9A8C3E0C64933271 CRC64;

Query Match 7.8%; Score 89.5; DB 2; Length 401;
Best Local Similarity 26.6%; Pred. No. 1.1;
Matches 42; Conservative 13; Mismatches 50; Indels 53; Gaps 6;

Oy 71 DLFTLKSTPSKSWAYL-----QVSKHLN-----NTKLSWNEDGTIH 108
Db 47 DAPPEIKSLPPKLLWLRLPMPSPSQRAKEVIQKHANFFDIIDRAQQGNLPSEK- 101
Oy 109 GLIYQDGNLIVQFGLYFIVCOLOFLVQ-----CSNHSVDLTQLLINSKIKQTLVTV 162
Db 102 --LKFNCTLVRSVGLYAFHQFOELQVQTNLNGNVPFKLLRLKLRKIKQKQN---- 155
Oy 163 CESGVQSKNYIYNLSQFLLHYLQVNSTISVRVDNFQIV 200
Db 156 -----QN---YLLSFQKADGIILNSDELAYV 179

RESULT 4
Q9WIS1 ID Q9WIS1 PRELIMINARY; PRT; 847 AA.
AC Q9WIS1;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE ENVELOPE GLYCOPROTEIN PRECURSOR, GPI60.
OC Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=97NOGIL3;
RA Jonassen T.O.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=97NOGIL3;
RX MEDLINE-20092438; PubMed-10628816;
RA Jonassen T.O., Grinde B., Asjo B., Hasle G., Hungnes O.;
RT "Inter-subtype recombinant HIV-1 involving HIV-MAL-like and subtype H-
RT like sequence in four Norwegian cases.";
RL AIDS Res. Hum. Retroviruses 16:49-58(2000).
DR EMBL: AJ237565; CAB39923.2; -
DR InterPro: IPR000328; -
DR InterPro: IPR000777; -
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
SQ SEQUENCE 847 AA; 95496 MW; E8770E4691304EB6 CRC64;

Query Match 7.8%; Score 89.5; DB 14; Length 847;
Best Local Similarity 20.9%; Pred. No. 2.4;
Matches 37; Conservative 37; Mismatches 56; Indels 47; Gaps 8;

Oy 52 DSTPNTTERKAPLKGNCSEDLFTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLI 111
Db 138 DTTNNTSIQPSQPSANCSEFNVTAIRDKQKVHALFYRV----DLVSIDNNDNNTYRLI 193
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```
QY 112 YDQGNLIYQ-----PGLYFIV-----COQLFYQCSNHSVD- 143
Db 194 NCNTSVITQACPKVTEPIPIHYCAPAGFAILKCNKNTKSGTGPCKNVSTVQCT-HGKIP 252
QY 144 -LTQLLLINSKIKKOTLVTVCSGVQSKNIYQNLQSLFLLHY----LQVNSTISVRVDN 196
Db 253 VVSTQLLINGSIAERVI-----IRSKNITDNTKNIIVHFNESVOINCT---RIAN 299

RESULT 5
Q9WV90 PRELIMINARY; PRT; 169 AA.
AC Q9WV90;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE FAS LIGAND (FRAGMENT).
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sclurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEALTHY LIVER;
RA Hodgson P.D., Grant M.D., Michalak T.I.;
RT "Perforin and Fas/Fas ligand-mediated cytotoxicity in acute and
RL chronic woodchuck viral hepatitis."
DR EMBL: AF152368; AAD38387.1; -.
DR InterPro: IPR000478; -.
DR Pfam: PF00229; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR SMART: SM00207; TNF; 1.
FT NON_TER 1
FT TER 169
SQ SEQUENCE 169 AA; 19274 MW; FDE395B014717B6B CRC64;
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```
Query Match 7.8%; Score 89; DB 11; Length 169;
Best Local Similarity 24.1%; Pred. No. 0.48; Mismatches 42; Indels 38; Gaps 7;
Matches 33; Conservative 24;

QY 78 STPSKKS---WAYLQVSKHLNNTKLSWNE---GTIHGLIYQDGNLIYQFPLXPIVQ 130
Db 32 SSPSDKKALRAAHLTKPNSRSPLEWDTYGISLSGVKYGKGLVINDTGLYFVYSK 91
QY 131 LQFLVQ-CSN----HSVDLTQLLINSK-----IKKQTLVTVCSG----- 166
Db 92 IYFRQSCNNQPLSHKV-----YVKNKYPQDLVLMCKRMNMYCTTGQMWARSYLGAVF 146
QY 167 --VQSKNIYQNLQSLFL 181
Db 147 NFTSNDHLIVNSELSL 163
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RESULT 6
Q28320 PRELIMINARY; PRT; 234 AA.
AC Q28320;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE TNF-ALPHA.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA Takakura H., Mori Y., Tatsumi M.;
```

```
RT "Molecular cloning of caprine TNF-alpha cDNA and its expression in
RT E.coli and insect cells.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: D86587; BAA13130.1; -.
DR HSSP: P01375; 4TSV.
DR InterPro: IPR000478; -.
DR InterPro: IPR003636; -.
DR Pfam: PF00229; TNF; 1.
DR PRINTS: PR01234; TNECROSISFCT.
DR PRODOM: PD002012; -.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS00049; TNF_2; 1.
DR SMART: SM00207; TNF; 1.
SQ SEQUENCE 234 AA; 25519 MW; 976BE33BBABB041 CRC64;

Query Match 7.7%; Score 88; DB 6; Length 234;
Best Local Similarity 24.1%; Pred. No. 0.84;
Matches 48; Conservative 38; Mismatches 89; Indels 24; Gaps 8;

QY 22 SRSFYLSITLALVCLVAVAILLVVYVKKDSTPTTTEKAPLKGNCSEDLFTLKST-- 79
Db 27 SRSWCWLSLFSF--LLVAGATTLLFCLLHFGVIGPQREEQSP-AGPSENRPLVQTLRSSQ 83
QY 80 -PSKKSWAYLQVSKHLNNTKLSWNEGT-----IHGLIYQDGNLIYQFPLXPIVQ 134
Db 84 ASSNKPVAVHY-VANISAPGQLRWGDSYANALKANGVELKNQLVVPTDGLYLIYSVLFR 142
QY 135 VQ-CSNHSVDLTQLLINSKIKKOTLVTVCS-----GVQSKNIYQNLQSLFLH 182
Db 143 GHGCPSTPLELT-HTISRIAVSYQTKVNILSAIKSPCHRETPEGAEPYPIYQGVF 201
QY 183 YLQVNSTISVRVDNFOYVD 201
Db 202 QLEKGDRLSAEQNPYLD 220

RESULT 7
Q9M9B0 PRELIMINARY; PRT; 896 AA.
AC Q9M9B0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE F27JJ15.13.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Brooks S., Buehler E., Chao O., Johnson-Hopson C., Khan S.,
RA Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howling B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsy N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F27JJ15 from chromosome
RT I.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -! SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AC016041; AAF69701.1; -.
DR InterPro: IPR000719; -.
DR InterPro: IPR001245; -.
DR InterPro: IPR001611; -.
DR InterPro: IPR002290; -.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00560; LRR; 3.
DR PRINTS: PR00019; LEURICHRPT.
DR PRINTS: PR00109; TYRKINASE.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
```

01-NOV-1996 (TRENBLrel: 01, Created)  
01-NOV-1996 (TRENBLrel: 01, Last sequence update)  
01-MAR-2001 (TRENBLrel: 16, Last annotation update)  
VESICLE COAT PROTEIN SEC16P.  
SEC16.  
Saccharomyces cerevisiae (Baker's yeast).  
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
Saccharomycetales; Saccharomycetaceae; Saccharomycetes;  
NCBI\_TaxID=4932;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=87089718; PubMed=3025612;  
RA Baker H.V.;  
RT "Glycolytic gene expression in Saccharomyces cerevisiae: nucleotide  
sequence of GCRL, null mutants, and evidence for expression.";  
RL Mol. Cell. Biol. 6:3774-3784(1986).  
[2]  
SEQUENCE FROM N.A.  
RA MEDLINE=88111651; PubMed=2892678;  
RX Velours J., Durrens P., Aigle M., Guerin B.;  
RT "ATP4, the structural gene for Yeast F0F1 ATPase subunit 4.";  
RL Eur. J. Biochem. 170:637-642(1988).  
[3]  
SEQUENCE FROM N.A.  
RA MEDLINE=92195335; PubMed=1312673;  
RX Davis J.L., Kunisawa R., Thorner J.;  
RT "A presumptive helicase (MOT1 gene product) affects gene expression  
and is required for viability in the yeast Saccharomyces cerevisiae.";  
RL Mol. Cell. Biol. 12:1879-1892(1992).  
[4]  
SEQUENCE FROM N.A.  
RA MEDLINE=95274317; PubMed=7754704;  
RX Schnall R., Mannhaupt G., Stucka R., Tauer R., Ehle S.,  
Schwarzlose C., Vetter I., Feldmann H.;  
RT "Identification of a set of yeast genes coding for a novel family of  
putative ATPases with high similarity to constituents of the 26S  
proteasome complex.";  
RL Yeast 10:1141-1155(1994).  
[5]  
SEQUENCE FROM N.A.  
RA MEDLINE=9528583; PubMed=7768896;  
RX Ledich S.D., Kostova Z., Latek R.R., Costello L.C., Drapp D.A.,  
Gray W., Fassler J.S., Orlean P.;  
RT "Temperature-sensitive yeast GPI anchoring mutants gpi2 and gpi3 are  
defective in the synthesis of N-acetylglucosaminyl  
phosphatidylinositol. Cloning of the GPI2 gene.";  
RL J. Biol. Chem. 270:13029-13035(1995).  
[6]  
SEQUENCE FROM N.A.  
RA MEDLINE=96017704; PubMed=7593161;  
RX Espenshade P., Gimeno R.E., Holzmacher E., Teung P., Kaiser C.A.;  
RT "Yeast SEC16 gene encodes a multidomain vesicle coat protein that  
interacts with Sec23p.";  
RL J. Cell Biol. 131:311-324(1995).  
[7]  
SEQUENCE FROM N.A.  
RA MEDLINE=97313271; PubMed=9169875;  
RX Bussey H., Storms R.K., Ahmed A., Alberman K., Allen E., Ansoorge W.,  
Araujo R., Aparicio A., Barrell B., Badcock K., Benes V., Botstein D.,  
Bowman S., Bruckner M., Carpenter J., Cherry J.W., Chung E.,  
Churche C., Coster F., Davis K., Davis R.W., Dietrich F.S.,  
Delius H., DiPaolo T., Dubois E., Dusterhoft A., Duncan M., Floeth M.,  
Fortin N., Friesen J.D., Fritz C., Goffeau A., Hall J., Hebling U.,  
Heumann K., Hilbert H., Hillier L., Hunnicke-Smith S., Hyman R.,  
Johnston M., Kalman S., Klein E., Komp C., Kurdi O., Lashkari D.,  
Lew H., Lin A., Lin D., Louis E.J., Marathe R., Messenguy F.,  
Mewes H.W., Mirtipati S., Moestl D., Muller-Auer S., Namath A.,  
Nentwich U., Oefner P., Pearson D., Petel F.X., Pohl T.M.,  
Purnelle D., Schafer M., Scharfe M., Scherens B., Schramm S.,  
Schroeder M., Sedu A.M., Tettelin H., Urrestazu L.A., Ushinsky S.,  
Vierdeels F., Vissers S., Voss H., Walsh S.V., Wambutt R., Wang Y.,  
Wedler E., Wedler H., Winnett E., Zhong W.W., Zollner A., Vo D.H.,  
Hani J.

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";  
 RN Nature 387:0-0(0).  
 [8]  
 RC SEQUENCE FROM N.A.  
 RA Hall J., Ahmed A., Bussey H., Fortin N., Friesen J.D., Storms R.K.,  
 Vo D.H., Wang Y., Winnett E.;  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 [9]  
 RN SEQUENCE FROM N.A.  
 RA Bussey H.;  
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.  
 [10]  
 RN SEQUENCE FROM N.A.  
 RA Jia Y., Cherry J.M.;  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U41849; AAB68254.1; -;  
 DR SGD; S0006006; SEC16.  
 SQ SEQUENCE 2195 AA; 241694 MW; 757B7A7231BEE6F0 CRC64;

Query Match 7.6%; Score 86.5; DB 3; Length 2195;  
 Best Local Similarity 20.9%; Pred. No. 13;  
 Matches 53; Conservative 39; Mismatches 87; Indels 75; Gaps 13;  
 QY 7 SVASPRSTRP-----WRSTSRSYF-----YLSSTALVCLVVA 39  
 DB 970 SVAPQENNPPIKDNEALLRRQPIIFHWSAANKVYAVPIPDQOYMISSIVQEIYV 1029  
 QY 40 VAILLVVQKDD---STNTTEKAPLKGNCSEDLFTLKSTPSKKS-----WAYLVQ 90  
 DB 1030 TPI--DQIIKPNMLKSPGPGLSAKLKKDLTKWETIKSISENESSDMDTWQLEEM 1087  
 QY 91 SKHLNNTKLSWNEGPIHGLIYODGNLV-----OFFGLY--FIVCOLQFL--VQ 136  
 DB 1088 KL---NDKVNWK---NISLLYNSDELLMYLSOPFPNGDMIPNAYRLDINCOMRVLAFLQ 1141  
 QY 137 CSNHSV-----DLTQLLINSIKKQTLVTV-----ESGVQSKNIYONLSQFLH 182  
 DB 1142 TGNHDEALRLAIKRDYAIALLVGLMGKDRWSEVIQYLYEGTAGPNDOKELAHFLL 1201  
 QY 183 YLQV---NSTISVR 193  
 DB 1202 IFQVFGNSKMAIK 1215

RESULT 10  
 Q9MYL6 PRELIMINARY; PRT; 280 AA.  
 AC Q9MYL6;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE FAS LIGAND.  
 GN PT-FASL OR CM-FASL OR RM-FASL.  
 OS Macaca nemestrina (Pig-tailed macaque),  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 OC NCBI\_TaxID=9545, 9541, 9544;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC SPECIES-M.nemestrina; STRAIN-PIG-TAILED MONKEY;  
 RA Kirli Y., Inoue T., Yoshino K.;  
 RT "Pig-tailed monkey Fas ligand mRNA, complete cds.";  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RN SEQUENCE FROM N.A.  
 RC SPECIES-M.fascicularis; STRAIN-CYNOMOLGUS MONKEY;  
 RA Kirli Y., Inoue T., Yoshino K.;  
 RT "Cynomolgus monkey Fas ligand mRNA, complete cds.";  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

[3]  
 RN SEQUENCE FROM N.A.  
 RC SPECIES-M.mulatta; STRAIN-RHESUS MONKEY;  
 RA Kirli Y., Inoue T., Yoshino K.;  
 RT "Rhesus monkey Fas ligand mRNA, complete cds.";  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB035140; BAA90296.1; -;  
 DR EMBL; AB035138; BAA90294.1; -;  
 DR EMBL; AB035139; BAA90295.1; -;  
 DR InterPro; IPR000478; -;  
 DR Pfam; PF00229; TNF\_1;  
 DR PRINTS; PR01234; TNFCROSISFCT.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50045; TNF\_2; 1.  
 SQ SEQUENCE 280 AA; 31367 MW; F0B284D61A132EB4 CRC64;

Query Match 7.5%; Score 86; DB 6; Length 280;  
 Best Local Similarity 21.3%; Pred. No. 1.6;  
 Matches 44; Conservative 35; Mismatches 64; Indels 64; Gaps 10;  
 QY 34 VCLVAVAVAILLVV-----QKQDSTPNTTEKAPLKGNCSEDLFTLKLS--- 78  
 DB 80 LCLLVFMFVLVALVGLGLGMFQLFHLQ-----ELAELESTSQKHTASSLEKQIG 131  
 QY 79 ----TPSKKSW---AYLOVSKHLNNTKLSWNEGDI---HGLIYODGNLIYVOPGLYFIV 128  
 DB 132 HPSPPPKKQKQVAHLTGKPNRSMPLEWEDTGVILLSGVYKKGGLVINETGLYEVY 191  
 QY 129 COLQFLQV-CSN---HSDVLTQLLINSK-----IKKQTLVTVCSG----- 166  
 DB 192 SKVTFRGQSCNPLSHKV-----YMRNSKYPQDLVMMKGMMSYCTTGQWHAHSSYLGA 246  
 QY 167 ----VQSKNIYONLSQFLHYLVQVNST 189  
 DB 247 VFNLTSADHLVNVSELSIVNFESQT 273

RESULT 11  
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 AC Q06629;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE SIMILARITY TO STREPTOCOCCUS PROTEIN V.  
 GN D9740.10 OR PLO2.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OC NCBI\_TaxID=4932;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,  
 Favell A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,  
 Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,  
 Johnston L., Langston Y., Latreille P., Le T., Mardis E., Meneses S.,  
 Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,  
 Taich A., Trevaskis E., Vignati D., Wilcox L., Wohlman P., Vaudin M.,  
 Wilson R., Waterston R.;  
 RA Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RN SEQUENCE FROM N.A.  
 RA Ding H.;  
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
 [3]  
 RN SEQUENCE FROM N.A.  
 RA Waterston R.;  
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RN SEQUENCE FROM N.A.  
 RA Jia Y., Cherry J.M.;  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

[illegible]

Search completed: September 5, 2001, 10:29:28  
Job time: 403 sec

QY 64 KGCNSEDLFCTLKST---PSKSMWAYLOVSKHLNNTKLSWNEDGT-----IHGLIYODGN 116  
Db 63 IGSMAQT---LTLRSSQSSDKPVAHV-VANHOVDQLEWLSRRANALLANGMDLKDNQ 118  
QY 117 LIVQPGPLYFVCQQLVQ-CSN-----HSVD-----LTLQLLINSKIKKQTLVT 161  
Db 119 LIVPADGLVLYVSOVLFKQGCSCNYLLLTHTVSFVAVSYEDKVNLLSAIKSPCKET--- 175  
QY 162 VCESGVQSKNIYONLSQFLHLHYLOVNSTISVRVDNFQYVD 201  
Db 176 --PEGSELKPWEPIYLGGVFQLEKGDRLSAEVLNPKYLD 213

## RESULT 15

081069  
ID O81069 PRELIMINARY; PRT; 884 AA.  
AC O81069;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE PUTATIVE RECEPTOR PROTEIN KINASE.  
GN T914.7.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
OC Brassicales; Brassicaceae; Arabidopsi.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. COLUMBIA;  
RA Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,  
RA Shen M., Renning C.M., Fraser C.M., Somerville C.R., Venter J.C.;  
RT "Arabidopsis thaliana chromosome II BAC T914 genomic sequence.";  
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL; AC005315; AAC33227.1; -.  
DR InterPro; IPR000719; -.  
DR InterPro; IPR000871; -.  
DR InterPro; IPR001611; -.  
DR InterPro; IPR002290; -.  
DR Pfam; PF00069; pkinase; 1.  
DR Pfam; PF00560; LRR; 2.  
DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR SMART; SM00220; S\_TKc; 1.  
KW ATP-binding; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 884 AA; 98755 MW; E354E899EAAE48BE CRC64;

Query Match 7.4%; Score 84.5; DB 10; Length 884;  
Best Local Similarity 25.1%; Pred. No. 7.6;  
Matches 52; Conservative 28; Mismatches 76; Indels 51; Gaps 12;  
QY 29 STTALVCLVAVAIILVVLVQKKDSTPNTTEKAPL-----KGCNC-SEDLFCTLKSTPSK 82  
Db 512 SAASLVVVVVA--LFFVRKKKSPSNLHAPSPVSNPGHNSQSESEF-----TSKK 564  
QY 83 KSWAYLOVSKHLNNTKLSWNEDG---TIHGLIYODGNLIVQFPGLYFVCQQLVQCSN 139  
Db 565 IRFTYSEVQEMTNFQKALGEGGFGVYVHGfV---NVIEQ-----VAVKLSQSSS 612  
QY 140 H-----SVDLTLQLLINSKIKKQTLVTVCESGVQSKNIYQ-----NLSQFLL-----H 182  
Db 613 QGYKHFAEVELLMRY---HHINLVSLVGYCDEGEHLALIYEYMPNGDLKQHLGSRKHGGF 669  
QY 183 YLQVNSTISVRVD---NFOYVDNTFTF 206  
Db 670 VLSWESRLKIVLDAALGLELYLHTGCVF 696



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2001, 10:29:51 ; Search time 19.38 Seconds  
(without alignments)  
388.865 Million cell updates/sec

Title: US-09-628-126-19

Perfect score: 1141

Sequence: 1 MQVQGSVASPWRSTRPWS.....DTNTPLDNLVSLYSSSD 220

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1141	100.0	239	1	TNF8_MOUSE
2	814.5	71.4	234	1	TNF8_HUMAN
3	109	9.6	279	1	FASL_MOUSE
4	91	8.0	278	1	FASL_RAT
5	88.5	7.8	309	1	41BL_MOUSE
6	87.5	7.7	235	1	TNFA_PERLE
7	86.5	7.6	2194	1	SC16_YEAST
8	85	7.4	291	1	TN10_MOUSE
9	84.5	7.4	233	1	TNFA_MACMU
10	84.5	7.4	525	1	C307_DROME
11	84	7.4	281	1	FASL_HUMAN
12	83.5	7.3	201	1	TNFB_MACEU
13	83.5	7.2	965	1	AMPN_MOUSE
14	82	7.2	234	1	TNFA_SHEEP
15	81.5	7.1	233	1	TNFA_CANFA
16	81.5	7.1	233	1	TNFA_MACFA
17	81	7.1	460	1	ENV_HV123
18	80.5	7.1	233	1	TNFA_FAPHU
19	80	7.0	1376	1	RPOD_ARATH
20	79	6.9	229	1	TNFA_CEREL
21	79	6.9	851	1	NUD1_YEAST
22	78.5	6.9	234	1	TNFA_HORSE
23	78.5	6.9	235	1	TNFA_RAT
24	78.5	6.9	1150	1	IRRI_YEAST
25	78	6.8	856	1	ENV_HV1MN
26	77.5	6.8	178	1	IL10_MACFA
27	77.5	6.8	463	1	YK3_YEAST
28	77.5	6.8	1583	1	MISA_SCHPO
29	77	6.7	795	1	SYFB_BUCAI
30	76.5	6.7	317	1	TN11_HUMAN
31	76.5	6.7	345	1	OPCM_BOVIN
32	76.5	6.7	507	1	C392_DROME
33	76.5	6.7	1073	1	HSER_PIG

34	76	6.7	234	1	TNFA_CAVPO
35	76	6.7	520	1	C4P2_DROME
36	75.5	6.6	178	1	IL10_CERTO
37	75.5	6.6	1178	1	PH81_YEAST
38	75	6.6	179	1	110H_HSV2
39	75	6.6	533	1	INV_DEBOC
40	75	6.6	2136	1	YCF2_MARPO
41	74.5	6.5	233	1	TNFA_HUMAN
42	74.5	6.5	284	1	YND3_YEAST
43	74.5	6.5	383	1	COS7_YEAST
44	74.5	6.5	488	1	CWF8_SCHPO
45	74.5	6.5	584	1	MUTL_BUCAI

## ALIGNMENTS

RESULT 1	
TNF8_MOUSE	
ID	TNF8_MOUSE
AC	P32972; STANDARD; PR7: 239 AA.
DT	01-OCT-1993 (Rel. 27, Created)
DT	01-OCT-1993 (Rel. 27, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	CD30 LIGAND (CD30-L).
GN	TNFSF8 OR CD30LG OR CD30L.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=T-cell;
RC	MEDLINE=93313964; Pubmed=8391931;
RA	Smith C.A., Gruess H.-J., Davis T., Anderson D., Farrah T.,
RA	Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA	Grabstein K.H., Gliniak B., McAllister I.B., Fanslow W., Alderson M.,
RA	Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.,
RT	"CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
RT	ligand defines an emerging family of cytokines with homology to
RT	TNF."
RT	Cell 73:1349-1360(1993).
CC	-1- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
CC	T CELLS.
CC	-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC	-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
CC	EMBL: L09754; AAA74595.1; -
DR	PIR: B40710; B40710.
DR	MGD: MGI:88328; Tnfsf8.
DR	InterPro: IPR000478; -
DR	Pfam: PF00229; TNF; 1.
DR	PROSITE: PS00251; TNF.1; 1.
DR	PROSITE: PS50049; TNF.2; 1.
KW	Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT	DOMAIN 1 43
FT	TRANSNEM 44 67
FT	DOMAIN 68 239
FT	FT CARBOHYD 75 75
FT	FT CARBOHYD 86 86
FT	FT CARBOHYD 114 114
FT	FT CARBOHYD 158 158
FT	FT CARBOHYD 194 194
FT	FT CARBOHYD 206 206
SQ	SEQUENCE 239 AA; 26519 MW; 29003157DD425159 CRC64;

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FT CARBOHYD      81      81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD     109     109 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD     153     153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD     189     189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD     201     201 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE      234 AA; 26017 MW; C653615682305B1B CRC64;

Query Match      71.4%; Score 814.5; DB 1; Length 234;
Best Local Similarity 70.6%; Pred. No. 6.8e-67;
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps

QY 1 MQVQPGSVASPRSTRPWRSTRSRFYFLSTTAL-VCLWVAIVAILLVQKKDSPNPTTE 59
Db 20 MHVPAGSVAS-----HLGTTTSRSFYELTTATLALCIUFTVATIMLVVQRTDTSIPNSPD 73
QY 60 KAPLPGGNCSEDLCTLAKSTPSKSWAYLOVSKHLNNTKLSWNEDGTFIHGLIVQDGNLIV 11
Db 74 NVPLPGGNCSEDLCLIKRAPFKSWAYLOVAKHLNNTKLSWNKDGILHGVRVQDGNLVI 13
QY 120 QPFGLYFYICQLQFLVQCNSHNSVDLTLLQLLINSIKKQTLVTVCSGVQSKNIYQNLQSF 17
Db 134 QPFGLYFYICQLQFLVQCNPNSVDLKLLELLINKHKKQALVTVCSGMQTKHVIYQNLQSF 19
QY 180 LLHYLQVNSTISVRVDNFQYVDTFNFPDLNDVLSVFLYSSSD 220
Db 194 LLDYLQVNTTISVNVDTFQYIDTSTFPLENVLSIFLYSNSD 234

RESULT 3
FASL_MOUSE
ID FASL_MOUSE STANDARD; PRT; 279 AA.
AC P41047; Q61217; Q9R1F2;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FAS ANTIGEN LIGAND.
GS TNFSF6 OR APTILG1 OR FASL OR GLD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=94185175; PubMed=7511063;
RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
RA Suda T., Nagata S.;
RT "Generalized lymphoproliferative disease in mice, caused by a point
RT mutation in the Fas ligand.";
RN Cell 76:969-976(1994).
RL [2]
RP SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
RC STRAIN=C57BL/6;
RX MEDLINE=95388076; PubMed=7544870;
RA Peitsch M.J., Tschopp J.J.;
RT "Comparative molecular modelling of the Fas-ligand and other members
RT of the TNF family.";
RL Mol. Immunol. 32:761-772(1995).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=95196085; PubMed=7889405;
RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a
RT TNF family gene cluster.";
RL Immunity 1:131-136(1994).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RC STRAIN=BALB/C;
RX Penner M.H., Shioda T., Isselbacher K.J.;
RA "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in
RA two amino acids.";
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases

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Query Match          9.68; Score 109; DB 1; Length 279;
Best Local Similarity 26.24; Pred. No. 0.0079;
Matches 37; Conservative 28; Mismatches 46; Indels 30; Gaps 7;

QY 78 STPSKK-----SWAYLOYSKHLNNTKLWNED-GT--IHGLLYODGNLIVOPFGLYFIWCQ 130
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 133 STPSEKPEPSVAHLTGNPHRSRISPLEWEDYGTALISGVKYKKGGLVINETGYLFVYSK 192
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 131 LQFIVQ-CSNHSVDLTQLQJLNSK-----IKKTQVLTVCSG-----VQ 168
    : | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 193 VYFRGSNNQPLNHKVYMR-NSKYPEDLVMEKRLNYCTTGQIWAHSSYLGAVENTLS 251
    : : | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 169 SKNIYQMSQFLHYLVQNST 189
    : : | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 252 ADHLYVNISQLSINFESKT 272
    : : | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 4
ID FASL_RAT STANDARD; PRT; 278 AA.
AC AC P36940;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FAS ANTIGEN LIGAND.
GN TNFSF6 OR APT1IC1 OR FASL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94084792; PubMed=7505205;
RA Suda T., Takahashi T., Golstein P., Nagata S.;
RT "Molecular cloning and expression of the Fas ligand, a novel member
RT of the tumor necrosis factor family.";
RL Cell 75:1169-1178(1993).
CC -1- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
CC TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
CC CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
CC PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
CC T CELLS, OR BOTH.
CC CC -1- SUBUNIT: HOMOTRIMER (PROBABLE).
CC CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
CC INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
CC SURFACE.
CC CC -1- TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND
CC THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES,
CC KIDNEY AND LUNG.
CC CC -1- INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.
CC CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC or send an email to licensel@isb-sib.ch).
CC -----
CC EMBL: U03470; AAC52129.1; -.
CC InterPro: IPR000478; -.
CC Pfam: PF00229; TNF_1.
CC DR PROSITE; PS00251; TNF_1; 1.
CC DR PROSITE; PS0049; TNF_2; 1.
CC KW Cytochrome; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis.
CC FT DOMAIN 1 77 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 78 99 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
CC FT DOMAIN 100 278 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 4 69 PRO-RICH.
CC FT DOMAIN 45 58 POLY-PRO.
CC FT DISULFID 199 230 BY SIMILARITY.

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Qy	78	STPSK-----KSWAYLQVSKHLNNTKLUSWED-GT---IHGLIYODGNLIWQFPGELFYVCQ	130
		: : : :   :   :   :   :   :   :   :	
Db	132	STPSETKKPRSAHLCNGNPRSRSIPLEWEDTYGTALISGVKYKGGLVINEAGLYFYYSK	191
		: : : :   :   :   :   :   :   :   :	
Qy	131	LQFLVQCSN-----HSV-----DLPLQLLLINSIKKQILVTTCVSGSVOSKNIIYNL	176
		:   :   :   :   :   :   :   :   :   :   :	
Db	192	VYFRGSCNSQPLSHKVYMRNKYPGDVLV-----EERKLNCTTG-----	233
Qy	177	SQELLHYLQWNSTISVRVDNFQYDVNTTFPLDN	209
		:   : : :   :   :   :   :   :   :   :	
Db	234	-QIAWHSYYLGAVENLTIVADHLVNIQSLSLN	265

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RESULT 6
TNFA_PERLE
ID TNFA_PERLE STANDARD; PRT; 235 AA.
AC P36939;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
GN TNF OR TNFA.
OS Peromyscus leucopus (White-footed mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=10041;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=92218012; Pubmed=1348497;
RX Crew M.D., Filipowsky M.E.;
RA "Sequence of the tumor necrosis factor/cachectin (TNF) gene from
RT Peromyscus leucopus (family Cricetidae).";
RL Immunogenetics 35:351-353(1992).
CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
CC EMBL; M59233; AAA0596.1; --
CC HSSP; P01375; 2TUN.
CC InterPro: IPR000478; --
CC InterPro: IPR002959; --

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Db 254 WLFPYQHLNKKI-INNS--STIRGFI-----MERIIRHRELSVDL 291
QY 145 -----TLQLLNSK-IKKOTLVTVCSGVSKNIYONLSQFLHLYLQVNSTISVR 193
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 292 DEPDRTFDALLKSLLEKQVSRNTIIFMLEDFIGGHSVGNLVMVLAYIAKNVDIGRR 351
QY 194 VD-----NQFYVNTNTP--LDNVLSVFLYSSS 219
      : : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 352 IQEBIDAIIEENRSINLLDMNAMPYTMATIFEVLYSSS 391

RESULT 11
FASL_HUMAN
ID FASL_HUMAN STANDARD; PRT; 281 AA.
AC P48023;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL).
GN TNFSF6 OR APTLIG1 OR FASL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127560; PubMed=7528780;
RA Alderson M.;
RT "Fas ligand mediates activation-induced cell death in human T
  lymphocytes.";
RL J. Exp. Med. 181:71-77(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127560; PubMed=7826947;
RA Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
RT "Human Fas ligand: gene structure, chromosomal location and species
  specificity.";
RL Int. Immunol. 6:1567-1574(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX Schaeetzlein C.E., Poehlmann R., Philippssen P., Eibel H.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=95071350; PubMed=7980502;
RA Mita E., Hayashi N., Iio S., Takehara T., Hijioaka T., Kasahara A.,
RA Fusanoto H., Kamada T.;
RT "Role of Fas ligand in apoptosis induced by hepatitis C virus
  infection.";
RL Biochem. Biophys. Res. Commun. 204:468-474(1994).
RN [5]
RP SEQUENCE FROM N.A.
RA Wilkinson J.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Blood;
RA Matsumura M., Nakanishi Y., Ohba Y.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases
CC -1- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
CC TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
CC CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
CC PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
CC T CELLS, OR BOTH.
CC -1- SUBUNIT: HOMOTRIMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
CC INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
CC SURFACE.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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100

RESULT	31
AMPN_MOUSE	
ID AMPN_MOUSE STANDARD; PRT;	965 AA.
AC	P97449;
DT	01-NOV-1997 (Rel. 35, Created)
DT	01-NOV-1997 (Rel. 35, Last sequence update)
DT	01-NOV-1997 (Rel. 35, Last annotation update)
DE	AMINOPEPTIDASE N [EC 3.4.11.2] (MICROSOMAL AMINOPEPTIDASE) (CD13)
DE	(P161 MEMBRANE PROTEIN).
DE	ANPEP OR LAP1.
GN	Mus musculus (Mouse).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxId=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=96399091; PubMed=8805662;
RA	Chen H., Kinzer C.A., Paul W.E.;
RT	"p161, a murine membrane protein expressed on mast cells and some
RT	macrophages, is mouse CD13/aminopeptidase N.";
RL	J. Immunol. 157:2593-2600(1996).
-!	CATALYTIC ACTIVITY: AMINOACYL-PEPTIDE + H(2)O = AMINO ACID + OLIGOPEPTIDE.
CC	-!- COFACTOR: BINDS ONE ZINC ION.
CC	





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DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
FT PROPEP 1 77
FT CHAIN 78 234 TUMOR NECROSIS FACTOR.
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DISULFID 146 178 BY SIMILARITY.
FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 63 63 MISSING (IN REF. 1).
SQ SEQUENCE 234 AA; 25536 MW; 4BCF8CCAB7956B88 CRC64;

Query Match 7.2%; Score 82; DB 1; Length 234;
Best Local Similarity 23.6%; Pred. No. 1.8;
Matches 47; Conservative 39; Mismatches 89; Indels 24; Gaps 8;

QY 22 SRSYFYLSTALVCLVAVAILVLVQVKDSTPNTEKAPLKGKGCSEDLFCTLKST-- 79
DB 27 SRSCWCLSLFSF--LLVAGATTFLCLLHFGVIGPQREQSP-AGPSFNRLPVQTLRSSQ 83
QY 80 -PSKSKWAYLOVSKHLNNTKLSWNEDGT----IHGLIYQDGNLIVOPGLYFIVCOLOFL 134
DB 84 ASNNKPAHV-VANISAPQLWGSYANALMANGVELDNQVLVPTDGLYLIYSQVLF 142
QY 135 VO-CSNHSVDLTQLLINSKIKKQTLVTVCES-----GVOSKNYQNLISQFLH 182
DB 143 GHGCPSTPLFLT-HTISRAVSYQTKVNLSAISKPSCHRETLEGAERAKPWYPIYGGVF 201
QY 183 YLOVNSTISVRVDNQYVD 201
DB 202 QLEKGRDLSAEINLPYLD 220

RESULT 15
TNFA_CANFA
ID TNFA_CANFA STANDARD; PRT; 233 AA.
AC P51742; Q28339;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
GN TNF OR TNFA.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Fiers W., Beernaert M.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Zucker K., Lu P., Fuller L., Asthana D., Esquenazi V., Miller J.;
RT "Cloning and expression of the cDNA for canine tumor necrosis
RT factor-alpha in E. coli.";
RL Lymphokine Res. 13:191-196(1994).
RN [3]
RP SEQUENCE OF 74-205 FROM N.A.
RC STRAIN-BEAGLE; TISSUE=Blood;
RA Gilmore W.H., Carter S.D., Bennett M., Barnes A., Kelly D.F.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -I- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -I- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING (BY SIMILARITY).
CC

-!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
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CC
CC EMBL; X94932; CAA64403.1; -
CC EMBL; S74068; AAB32391.1; -
CC EMBL; Z70046; CAA93908.1; -
CC HSP; P01375; TNF.
CC InterPro; IPR000478; -
CC InterPro; IPR002959; -
CC Pfam; PF00229; TNF; 1.
CC PRINTS; PR01234; TNECROSISFCT.
CC PRINTS; PR01235; TNFALPHA.
CC PROSITE; PS00251; TNF_1; 1.
CC PROSITE; PS50049; TNF_2; 1.
CC Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
FT PROPEP 1 76 POTENTIAL.
FT CHAIN 77 233 TUMOR NECROSIS FACTOR.
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DISULFID 145 177 BY SIMILARITY.
FT CONFLICT 59 60 QR -> PE (IN REF. 2).
FT CONFLICT 66 66 G -> C (IN REF. 2).
FT CONFLICT 74 74 A -> V (IN REF. 3).
FT CONFLICT 111 111 A -> D (IN REF. 2).
FT CONFLICT 116 116 G -> D (IN REF. 2).
FT CONFLICT 134 135 IY -> DS (IN REF. 2).
SQ SEQUENCE 233 AA; 25447 MW; 7B2568FBC8B25340 CRC64;

Query Match 7.1%; Score 81.5; DB 1; Length 233;
Best Local Similarity 23.6%; Pred. No. 2;
Matches 48; Conservative 32; Mismatches 90; Indels 33; Gaps 9;

QY 22 SRSYFYLSTALVCLVAVAILVLVQVKDSTPNTEKAPLKGKGCSEDLFCTLK 77
DB 27 SRRCFCLSLFSFLVAVAGATTFLCLLHFGVIGPQRELPN-----GLQLISPLAQTVK 78
QY 78 S---TPSKKSWAYLOVSKHLNNTKLSWNEDGT-----IHGLIYQDGNLIVQPGLYFIVCQ 130
DB 79 SSRTPSDKPAHVAVANPEAG-QLWLSRRANALLANGVELTDNQLIVPSDGLYLIYSQ 137
QY 131 LOFLVO-CSNHSVDLTQLLINSKIKKQTLVTV-----CE-----SQVOSKNYQNLISQ 178
DB 138 VLKPGOGCPSTHVLTT-HTISRAVSYQTKVNLSAISKPSQRETPTGTEAKPWYPIYL 196
QY 179 FLHLHYQVNSTISVRVDNQYVD 201
DB 197 GGVFQLEKGRDLSAEINLPYLD 219

Search completed: September 5, 2001, 10:29:52
Job time: 397 sec
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2001, 10:23:51 : Search time 31.97 seconds  
(without alignments)  
524.191 Million cell updates/sec

Title: US-09-628-126-19  
Perfect score: 1141  
Sequence: 1 MQVPGSVASPRWRSRPRWS.....DTNTFPLDNVLSVFLYSSD 220

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1141	100.0	239	2 A40710	CD30 ligand - mous
2	814.5	71.4	234	2 A40710	CD30 ligand - huma
3	109	9.6	279	2 A53062	Fas ligand - mouse
4	91	8.0	278	2 A49266	Fas ligand - rat
5	89.5	7.8	401	2 S74767	hypothetical prote
6	88.5	7.8	309	2 I53384	4-1BB ligand - mou
7	87.5	7.7	235	2 I54490	tumor necrosis fac
8	87	7.6	2013	2 C71610	probable membrane
9	86.5	7.6	2195	2 S61103	SEC16 protein - ye
10	86	7.5	674	2 S61181	hypothetical prote
11	85.5	7.5	994	2 H96510	probable disease r
12	84.5	7.4	884	2 T02731	serine/threonine-s
13	84	7.4	281	2 I38707	Fas ligand - huma
14	84	7.4	1110	2 F84547	probable disease r
15	82	7.2	234	1 JH0529	tumor necrosis fac
16	81.5	7.1	304	2 T27593	hypothetical prote
17	81.5	7.1	304	2 T27594	hypothetical prote
18	81	7.1	866	2 T10587	serine/threonine-s
19	80.5	7.1	344	2 T05104	hypothetical prote
20	80	7.0	165	2 H64460	hypothetical prote
21	80	7.0	369	2 S77028	protein kinase, 41
22	79.5	7.0	889	2 T45691	receptor-like prot
23	79	6.9	851	2 S67285	NUD1 protein - yea
24	78.5	6.9	234	1 JQ1344	tumor necrosis fac
25	78.5	6.9	235	2 JU0029	tumor necrosis fac
26	78.5	6.9	1150	2 S49956	probable membrane
27	78	6.8	427	2 T40064	hypothetical prote
28	78	6.8	616	2 T32131	hypothetical prote
29	78	6.8	859	1 VCLJMN	env polyprotein pr

30	77.5	6.8	463	2 S37962	probable purine nu
31	77.5	6.8	1583	2 S59644	sister chromatid c
32	77	6.7	428	2 T48284	hypothetical prote
33	77	6.7	568	2 T20421	hypothetical prote
34	77	6.7	769	2 T39089	hypothetical prote
35	77	6.7	795	2 H84944	phenylalanine--L-RN
36	76.5	6.7	345	2 S03199	opioid-binding pro
37	76.5	6.7	1083	2 A38919	hypothetical prote
38	76.5	6.7	1223	2 T17345	hypothetical prote
39	76	6.7	205	2 H71639	NADH dehydrogenase
40	76	6.7	665	2 T06082	protein kinase hom
41	76	6.7	1313	2 G82887	hypothetical prote
42	75.5	6.6	208	2 B86877	ABC transporter At
43	75.5	6.6	251	2 T25121	hypothetical prote
44	75.5	6.6	303	2 T25114	hypothetical prote
45	75.5	6.6	659	2 T49277	hypothetical prote

ALIGNMENTS

RESULT 1  
B40710  
CD30 ligand - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 05-Nov-1999  
C:Accession: B40710  
R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland, Alderson, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, Cell 73, 1349-1360, 1993  
A:Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de  
A:Reference number: A40710; MUID:93313964  
A:Accession: B40710  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-239 <SM>  
A:Cross-references: GB:L09754; NID:g349288; PIDN:AAA74595.1; PID:g349289  
C:Keywords: cytokine receptor; membrane protein; surface antigen

Query Match	100.0%	Score 1141;	DB 2;	Length 239;
Best Local Similarity	100.0%	Pred. No. 1.8e-96;		
Matches 220;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MQVPGSVASPRWRSRPRWRSFYLSLTALVCLVAVAILLVVQKDDSTPNTTEK	60	
Db	20	MQVPGSVASPRWRSRPRWRSFYLSLTALVCLVAVAILLVVQKDDSTPNTTEK	79	
Qy	61	APLGGNGSEDLFCTLKSTPSKSWAYLOVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQ	120	
Db	80	APLGGNGSEDLFCTLKSTPSKSWAYLOVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQ	139	
Qy	121	FPGLYFVLCQLQFLVQCSNHSVDLTLQLLINSKIKQTLVTVCESGVSKNIYQNLQFL	180	
Db	140	FPGLYFVLCQLQFLVQCSNHSVDLTLQLLINSKIKQTLVTVCESGVSKNIYQNLQFL	199	
Qy	181	LHYLQVNSTISVRVDNFQYVDNTFPLDNVLSVFLYSSD	220	
Db	200	LHYLQVNSTISVRVDNFQYVDNTFPLDNVLSVFLYSSD	239	

RESULT 2  
A40710  
CD30 ligand - human  
C:Species: Homo sapiens (man)  
C>Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 21-Jul-2000  
C:Accession: A40710  
R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland, Alderson, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, Cell 73, 1349-1360, 1993  
A:Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de  
A:Reference number: A40710; MUID:93313964  
A:Accession: A40710



C;Accession: C71610  
R.;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.O.; Koonin, E.H.  
; Perle, M.J.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.  
Science 282, 1126-1132, 1998  
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.  
A;Reference number: A71600; MUID:99021743  
A;Accession: C71610  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-2013 <GAR>  
A;Cross-references: GB:AE001406; GB:AE001362; NID:g3845230; PIDN:AAC71912.1; PID:g384  
A;Experimental source: clone 3D7  
C;Genetics:  
A;Gene: PFB0615c

Query Match 7.6%; Score 87; DB 2; Length 2013;  
Best Local Similarity 23.9%; Pred. No. 18; Indels 28; Gaps 7;  
Matches 34; Conservative 31; Mismatches 49;

Qy 69 SEDLFTCLKTPSKKWAYLQVSKHLNNKLNSWNEDGTIHGLIYQDGNLVQPFGLYFIY 128  
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :  
Db 16 SDNIFCFLKD-----GYICFMNLN-----NEKKYLITCSQDSGYAQY---YFDV 59

Qy 129 COLQFLVOCSNHVSVDLPQLLI-----NSKKTKQTPLVTVCESGVOSKNIYNLSQFL--- 181  
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :  
Db 60 VKCRYEKKECDCKNMNTIMLLQNENKIITKCYI---KNVVTKNIYHTL--FLWINK 114

Qy 182 HYLOVNSTISVRVDNFQYVDTN 203  
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :  
Db 115 HYHNILCSLSPENNSSFELMTN 136

RESULT 9  
S61103  
SEC16 protein - yeast (Saccharomyces cerevisiae)  
N;Alternate names: protein LPF1w; protein YPL085w  
C;Species: Saccharomyces cerevisiae  
C;Date: 23-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 06-Feb-1998  
C;Accession: S61103  
R;Hall, J.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.; Vo, D.H.;  
submitted to the EMBL Data Library, August 1995  
A;Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.  
A;Reference number: S59677  
A;Accession: S61103  
A;Molecule type: DNA  
A;Residues: 1-2195 <HAL>  
A;Cross-references: EMBL:U41849; NID:g1147608; PID:g1147609; MIPS:YPL085w  
C;Genetics:  
A;Gene: SGD:SEC16  
A;Cross-references: SGD:S0006006; MIPS:YPL085w  
A;Map position: 16L  
C;Keywords: transmembrane protein  
F;1198-1214/Domain: transmembrane #status predicted <TM1>  
F;1250-1266/Domain: transmembrane #status predicted <TM2>

Query Match 7.6%; Score 86.5; DB 2; Length 2195;  
Best Local Similarity 20.9%; Pred. No. 22; Indels 75; Gaps 13;  
Matches 53; Conservative 39; Mismatches 87;

Qy 7 SVASPPWRSTRP-----WRSTSRSYF-----YLTSTALVCLWA 39  
| | | | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :  
Db 970 SVAPROENNPDKINEALLRRQPFIEHSAANKVAVVPPIPDQSQMYSSTIVQEIKV 1029

Qy 40 VAILVLVVKRK---STPNPTEKAPLKGNCSEDLCTLKTSPSKKS-----WAYLQV 90  
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :  
Db 1030 TPI--DQIIKPNDMLKFPFGPLGSALKKKDLTKWMETTIKSIENESBDMTWTQLEEM 1087

Qy 91 SKHLNNTKLSWNEDGTIHGLIYQDGNLV-----QFPGLY--FIVCOQLF--VQ 136  
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :  
Db 1088 KL--NDKVNVK----NISKULYNSDELLMYLSQFPFGMDIMPAYRLDINCOMRVLAFLQ 1141

```
QY 137 CSNHSV-----DLTQLLINSKIKKOTLVTV-----ESGVQSKNIYONLSQFLH 182
||| : ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1142 TGNHDLRALSLKALYATALLVGLMGKDRWSEVIOKYLYEGFTAGPNDQKELAHFLL 1201

QY 183 YLQV---NSTISVR 193
||| : ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1202 IFQVFGNSKMAIK 1215

RESULT 10
S61181
N:Alternate names: hypothetical protein YDR295c - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 23-Mar-2001
C:Accession: S61181
R:Ding, H.
submitted to the EMBL Data Library, June 1995
A:Description: The sequence of S. cerevisiae cosmid 9740.
A:Reference number: S61160
A:Accession: S61181
A:Molecule type: DNA
A:Residues: 1-674 <DIN>
A:Cross-references: EMBL:U28374; NID:g849207; PID:g849217; GSPDB:GN00004; MIPS:YDR295c
C:Genetics:
A:Gene: MIPS:YDR295c
A:Map position: 4R

Query Match 7.5%; Score 86; DB 2; Length 674;
Best Local Similarity 25.0%; Pred. No. 6;
Matches 40; Conservative 30; Mismatches 60; Indels 30; Gaps 9;

QY 51 KDSTPNTTEKAPLKGNC-----EDLEFCTLKSPSK-----SWAYLQVSKHLNTRK- 98
||| : ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 192 KDGTPNSVSSSTSSNSYSYTGSKDDYDYSVKRNLKRKRINTDDWLFATTKHLKHQY 251

QY 99 LSWNDGDIHGLIYQDGNLIVQFPGLYFI-----VCOLOQLVQCSNHSVDLTQLLIN 151
||| : ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 252 LLANYD--IDMIISFDPMLEVPALQVLRNANKDIPKILVQ---NSPD---HYLLD 303

QY 152 SKIRKQTLVT---VCESG-VQSKNIYONLSQFLHYLQVNS 188
||| : ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 304 SEIRNSSYKSHLSNNGHVDSDQEEIEKSSLLYFLQARN 343

RESULT 11
H96510
Probable disease resistance protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: H96510
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chlin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: H96510
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-994 <STO>
A:Cross-references: GB:AE005173; NID:g11321768; PIDN:AAG34245.1; GSPDB:GN00141
C:Genetics:
A:Gene: F2G19.6
A:Map position: 1
```

```
Query Match 7.5%; Score 85.5; DB 2; Length 994;
Best Local Similarity 26.3%; Pred. No. 11;
Matches 40; Conservative 21; Mismatches 64; Indels 27; Gaps 8;

QY 88 LQVSKHLNNTKLSWNE-DGTIHGLI-----YQDGNLIVQFPGLYFIYVQLOFLVQ 136
||| : ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 322 LRSLSLNSLVLSENNFFVEIPSSVSNLKQLTLFDVSDNNLNGNFFPSLLNLNLQRLYDI 381

QY 137 CSNHSVDLTQLLINSKIKKOTLVTVCSGVQSK-----NIYONLSQFLHYLQVNSTI 190
||| : ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 382 CSNHTGFLPPTI--SQLSNLEFFSACDNSTGSPSSLPNI--SLTLGLSLYNOLNDTT 438

QY 191 SVR-----VDNFQ--YVDNTNTEPLDNV-LSVEL 215
||| : ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 439 NIKNISLHLNLQRLLEDNNNFKAQVDLDVFL 470

RESULT 12
T02731
serine/threonine-specific protein kinase (EC 2.7.1.1-) T914.7 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Feb-2001
C:Accession: T02731; D84691
R:Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M.;
submitted to the EMBL Data Library, August 1998
A:Description: Arabidopsis thaliana chromosome II BAC T914 genomic sequence.
A:Reference number: 214710
A:Accession: T02731
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-884 <ROU>
A:Cross-references: EMBL:AC005315; NID:g3461834; PIDN:AAC33227.1; PID:g3461841; GSPDB
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
eaus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
ature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: D84691
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-884 <STO>
A:Cross-references: GB:AE002093; NID:g3461841; PIDN:AAC33227.1; GSPDB:GN00139
C:Genetics:
A:Gene: ATSP:T914.7; At2g28990
A:Map position: 2
A:Introns: 24/1; 203/2; 362/1; 410/2; 434/2; 458/2; 484/2; 538/1; 621/3; 664/1; 686/1
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase
C:Keywords: phosphotransferase; protein kinase

Query Match 7.4%; Score 84.5; DB 2; Length 884;
Best Local Similarity 25.1%; Pred. No. 11;
Matches 52; Conservative 28; Mismatches 76; Indels 51; Gaps 12;

QY 29 STTALVCLVAVAILVLVQKDKSTPTTEKAPL-----KGGNC-SEDLFCTLKSTPSK 82
||| : ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 512 SAASLVVIVVVA--LFFVFRKKKSNLHAPPSVNPNGNSQSESSF-----TSKK 564

QY 83 KSWAYLQVSKHLNNTKLSWNEG---TIHGLIYQDGNLIVQFPGLYFIYVQLOFLVQCSN 139
||| : ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 565 IRTYSEVQEMTNFDKALGEGGFGVYHGFV---NVIEQ-----YAVKLLSSSS 612

QY 140 H-----SVDLTQLLINSKIKKOTLVTVCSGVQSKNIYQ-----NLSQFL-----H 182
||| : ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 613 QGYKHEFAEVELLMRV---HHINLVSLVGYCDEGEHALIYETMPNGDLKQHLGSKHGFG 669

QY 183 YLQVNSTISVRVD---NFQYVDNTNTP 206
||| : ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 670 VLSWESRLKIVLDAALGLELYLHTGCV 696
```

```
RESULT 13
138707
Fas ligand - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: 138707; JC2340; S57565; 138554
R: Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.
Int. Immunol. 6, 1567-1574, 1994
A:Title: Human Fas ligand: gene structure, chromosomal location and species specificity.
A:Reference number: 138707; MUID:95127560
A:Accession: 138707
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-281 <RES>
A:Cross-references: EMBL:U11821; NID:g9595430; PIDN:AAC50124.1; PID:g9595431
R: Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioaka, T.; Kasahara, A.; Fusamoto, H.;
Biochem. Biophys. Res. Commun. 204, 468-474, 1994
A:Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
A:Reference number: JC2340; MUID:95071350
A:Accession: JC2340
A:Molecule type: DNA
A:Residues: 1-281 <MIT>
A:Cross-references: GB:D38122; DBJ:D29820; NID:g601892; PIDN:BAA07320.1; PID:g1369902
R: Schatzlein, C.E.
submitted to the EMBL Data Library, June 1995
A:Reference number: S57565
A:Accession: S57565
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-281 <SCH>
A:Cross-references: NID:g887455; PID:g887456
R: Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; Go
J. Exp. Med. 181, 71-77, 1995
A:Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A:Reference number: 138554; MUID:95105731
A:Accession: 138554
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-281 <RE2>
A:Cross-references: EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PID:g624628
C:Genetics:
A:Gene: FasL
A:Introns: 151/1; 116/3
C:Keywords: glycoprotein; transmembrane protein
F:80-102/Domain: transmembrane #status predicted <TMM>
F:76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.4%; Score 84; DB 2; Length 281;
Best Local Similarity 20.3%; Pred. No. 3.3;
Matches 42; Conservative 36; Mismatches 65; Indels 64; Gaps 9;

QY 34 VCLWVAATILVLWV-----OQKDDSTPNTTEKAPLKGNGCEDLFC 74
Db 81 LCLLVNFFWLVVALVGLGMLGFHLOKELARESTSQMHTASSLEKQIGHPS----- 135
QY 75 TLKSTPSKSW---AYLQVSKHLNNTKLSWNEGTI---HGLIYQDGNLIIVQFPLGYFIV 128
Db 136 ---PPPEKELRKAHLTGKNSRSRMPLEWEDTYGIVLLSGVKYKKGGLVNETGLYFVY 192
QY 129 COLQFLVQ-CSN-----HSVDLTQLQLINSK-----IKKQTLVTVCSG----- 166
Db 193 SKVYFRGQSCNPLPLSHKV-----YMRNSKYPDVLVMECKMMSYCTTGQMWARSVSLGA 247
QY 167 ----VQSKNIYQNLSFLHLYLVNST 189
Db 248 VFNLTSADHLVNVSELSLVNFEESQT 274

RESULT 14
F84547
probable disease resistance protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
```

```
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: F84547
R: Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: F84547
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1110 <STO>
A:Cross-references: GB:AE002093; NID:g6598362; PIDN:AAF18600.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g17060
A:Map position: 2

Query Match 7.4%; Score 84; DB 2; Length 1110;
Best Local Similarity 22.7%; Pred. No. 16;
Matches 44; Conservative 36; Mismatches 66; Indels 48; Gaps 10;

QY 27 YLSTTALVCLVAV---AIIIV-----LVVQKKDSTPNTTEKAPLKGNGCEDLFC 76
Db 680 YLQGTAKICPTSIENLOKLIIILLDKCEVIVSLPDLCLGNLSLQELILSGCSK-----L 734
QY 77 KSTPSKSWAYLQVSKHLNNTKLSWNEGTI---HGLIYQDGNLIIVQFPLGYFIVCOLQFLVQ 136
Db 735 KFFPELK-----ETMKSIK-----ILLDDGTAKOMPIL---LQC-----IQ 768
QY 137 CSNHSV-DLTQLLINSKIKKQTLVTVCSGVQSKNIYQNLSQ-FLHLYLVNST----- 189
Db 769 SGHVSVAKNTLPNSLDYLYPSSLISLCLSGNDIESLHANISQLYHLKWLKLDLKNCKLKS 828
QY 190 ISVRVDNFQYVDN 203
Db 829 VSLPPNLKCLDAH 842

RESULT 15
JH0529
tumor necrosis factor alpha precursor - sheep
N:Alternate names: cachectin; TNF alpha
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: JH0529; S48118; S13114; S20661
R: Green, I.R.; Saigan, D.R.
Gene 109, 203-210, 1991
A:Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems wi
A:Reference number: JH0529; MUID:92112044
A:Accession: JH0529
A:Molecule type: mRNA
A:Residues: 1-234 <GRE>
A:Cross-references: EMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406
R: Nash, A.D.; Barcham, G.J.; Brandon, M.R.; Andrews, A.E.
Immunol. Cell Biol. 69, 273-283, 1991
A:Title: Molecular cloning, expression and characterization of ovine TNF-alpha.
A:Reference number: S48118; MUID:92155784
A:Accession: S48118
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-234 <NAS>
A:Cross-references: EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PID:g297807
R: Young, A.J.; Hay, J.B.; Chan, J.Y.C.
Nucleic Acids Res. 18, 6723, 1990
A:Title: Primary structure of ovine tumor necrosis factor alpha cDNA.
A:Reference number: S13114; MUID:91067496
A:Accession: S13114
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-62,64-234 <YOU>
A:Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404
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A:Note: comparison with the introns of homologous sequences suggest that this is probably  
C:Superfamily: tumor necrosis factor  
C:Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein; lymph  
F:1-77/Domain: propeptide #status predicted <PRO>  
F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>  
F:20/Binding site: myristate (Lys) (covalent) #status predicted  
F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted  
F:96/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:146-178/Disulfide bonds: #status predicted

Query Match	7.2%	Score 82;	DB 1;	Length 234;
Best Local Similarity	23.6%	Pred. No. 4;		
Matches 47;	Conservative 39;	Mismatches 89;	Indels 24;	Gaps 8;
Qy 22	SRSYFVLTALVCLVAVAILLVLVVQKDSPTNTTEKAPLKGNCSEDLFCTLKST--	79		
Db 27	SRSCWCLSLFSP--LLVAGATTFLCLLHFGVIGPQREEQSP-AGPSFNRPVQTLRSSQ	83		
Qy 80	-PSKKSWAYLVQVSKHLNNTKLSWNEDGT----IHGLIYQDGNLIVQPGLYFIVCOLQFL	134		
Db 84	ASNKKPVAHV-VANISAPQLRWGDSYANALMANGVELKDNLVVPVTDGLYLIYSQVLF	142		
Qy 135	VQ-CSNHSVDLPLQLLINSKIKKQTLVTVCES-----GVOSKNYIQNLSQFLH	182		
Db 143	GHGCPSTPLFLT-HTISRIAVSYQTKVNILSAIKSPCHRETLEGAEAKPWYEPYOGGVF	201		
Qy 183	YLOVNSTISVRVDNFQYVD	201		
Db 202	QLEKGDRLSAEINLPEYLD	220		

Search completed: September 5, 2001, 10:23:52  
Job time: 122 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2001, 10:23:10 ; Search time 25.09 Seconds  
(without alignments)  
180.545 Million cell updates/sec

Title: US-09-628-126-19  
Perfect score: 1141  
Sequence: 1 MQVPGSVASWRTRPWS.....DTNTPPLDNLVFLYSSD 220

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5b\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1141	100.0	220	1 US-08-225-989-19	Sequence 19, Appl
2	1141	100.0	220	1 US-08-570-923-19	Sequence 19, Appl
3	1141	100.0	220	1 US-08-580-014-19	Sequence 19, Appl
4	1141	100.0	220	4 US-09-079-785-19	Sequence 19, Appl
5	1141	100.0	239	1 US-08-225-989-6	Sequence 6, Appl
6	1141	100.0	239	1 US-08-570-923-6	Sequence 6, Appl
7	1141	100.0	239	1 US-08-580-014-6	Sequence 6, Appl
8	1141	100.0	239	4 US-09-079-785-6	Sequence 6, Appl
9	814.5	71.4	215	1 US-08-225-989-23	Sequence 23, Appl
10	814.5	71.4	215	1 US-08-570-923-23	Sequence 23, Appl
11	814.5	71.4	215	1 US-08-580-014-23	Sequence 23, Appl
12	814.5	71.4	215	4 US-09-079-785-23	Sequence 23, Appl
13	814.5	71.4	234	1 US-08-225-989-8	Sequence 8, Appl
14	814.5	71.4	234	1 US-08-570-923-8	Sequence 8, Appl
15	814.5	71.4	234	1 US-08-580-014-8	Sequence 8, Appl
16	814.5	71.4	234	4 US-09-079-785-8	Sequence 8, Appl
17	685	60.0	130	1 US-08-225-989-21	Sequence 21, Appl
18	685	60.0	130	1 US-08-570-923-21	Sequence 21, Appl
19	685	60.0	130	1 US-08-580-014-21	Sequence 21, Appl
20	685	60.0	130	4 US-09-079-785-21	Sequence 21, Appl
21	624	54.7	148	3 US-08-584-031-12	Sequence 12, Appl
22	388.5	34.0	125	1 US-08-225-989-20	Sequence 20, Appl
23	388.5	34.0	125	1 US-08-570-923-20	Sequence 20, Appl
24	388.5	34.0	125	1 US-08-580-014-20	Sequence 20, Appl
25	388.5	34.0	125	4 US-09-079-785-20	Sequence 20, Appl
26	229	20.1	52	4 US-09-369-494-17	Sequence 17, Appl
27	104	9.1	279	5 PCT-US95-00362-5	Sequence 5, Appl

RESULT 1  
US-08-225-989-19  
; Sequence 19, Application US/08225989  
; Patent No. 5480981  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jürgen  
; TITLE OF INVENTION: No. 5480981 Cytochrome That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644

## ALIGNMENTS

28 88.5 7.8 309 1 US-08-236-918A-2 Sequence 2, Appli  
29 85 7.4 291 1 US-08-670-354-6 Sequence 6, Appli  
30 85 7.4 291 5 PCT-US96-10895-6 Sequence 6, Appli  
31 84 7.4 281 2 US-08-810-453-2 Sequence 2, Appli  
32 84 7.4 281 3 US-08-815-190A-2 Sequence 2, Appli  
33 84 7.4 281 4 US-09-290-640-25 Sequence 25, Appli  
34 84 7.4 281 4 US-09-479-524-3 Sequence 3, Appli  
35 84 7.4 281 5 PCT-US95-00362-2 Sequence 2, Appli  
36 83.5 7.3 287 3 US-08-815-190A-16 Sequence 16, Appli  
37 83 7.3 550 2 US-08-417-210A-140 Sequence 140, App  
38 83 7.3 551 2 US-08-417-210A-137 Sequence 137, App  
39 83 7.3 551 2 US-08-417-210A-143 Sequence 143, App  
40 83 7.3 857 1 US-08-022-835-4 Sequence 4, Appli  
41 83 7.3 857 1 US-08-388-809-4 Sequence 4, Appli  
42 83 7.3 857 2 US-08-647-714-4 Sequence 8, Appli  
43 82.5 7.2 183 4 US-09-105-343A-8 Sequence 10, Appl  
44 80.5 7.1 233 1 US-08-323-445A-10 Sequence 10, Appl  
45 80.5 7.1 233 1 US-08-515-903A-10 Sequence 10, Appl

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;
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 220 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-225-989-19

Query Match          100.0%; Score 1141; DB 1; Length 220;
Best Local Similarity 100.0%; Pred. No. 2.1e-110;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQVQPGSVASPRWSTPRWSTRSYFYLTSTALVCLVAVAILLVLVVQKDKSTPNTTEK 60
Db 1 MQVQPGSVASPRWSTPRWSTRSYFYLTSTALVCLVAVAILLVLVVQKDKSTPNTTEK 60
QY 61 APLKGGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQ 120
Db 61 APLKGGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQ 120
QY 121 FPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQTLVTVCSGVQSKNIYQNLSQL 180
Db 121 FPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQTLVTVCSGVQSKNIYQNLSQL 180
QY 181 LHYLQVNSTISVRVDFNFQYVDNTFPLDNVLSVFLYSSSD 220
Db 181 LHYLQVNSTISVRVDFNFQYVDNTFPLDNVLSVFLYSSSD 220

RESULT 2
US-08-570-923-19
; Sequence 19, Application US/08570923
; Patent No. 5677430
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,923
; FILING DATE: 12-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
```

```
;
;
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 220 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-570-923-19

Query Match          100.0%; Score 1141; DB 1; Length 220;
Best Local Similarity 100.0%; Pred. No. 2.1e-110;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQVQPGSVASPRWSTPRWSTRSYFYLTSTALVCLVAVAILLVLVVQKDKSTPNTTEK 60
Db 1 MQVQPGSVASPRWSTPRWSTRSYFYLTSTALVCLVAVAILLVLVVQKDKSTPNTTEK 60
QY 61 APLKGGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQ 120
Db 61 APLKGGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQ 120
QY 121 FPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQTLVTVCSGVQSKNIYQNLSQL 180
Db 121 FPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQTLVTVCSGVQSKNIYQNLSQL 180
QY 181 LHYLQVNSTISVRVDFNFQYVDNTFPLDNVLSVFLYSSSD 220
Db 181 LHYLQVNSTISVRVDFNFQYVDNTFPLDNVLSVFLYSSSD 220

RESULT 3
US-08-580-014-19
; Sequence 19, Application US/08580014
; Patent No. 5753203
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,014
; FILING DATE: 20-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
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CLASSIFICATION: 530  
PRIOR APPLICATION DATA: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 220 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-580-014-19

Query Match 100.0%; Score 1141; DB 1; Length 220;  
Best Local Similarity 100.0%; Pred. No. 2.le-110;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MQVPGSVASPRWSTPRWSTRSFYLSLTALVCLVAVAILLVVQVKDSTPNTTEK 60  
DB 1 MQVPGSVASPRWSTPRWSTRSFYLSLTALVCLVAVAILLVVQVKDSTPNTTEK 60  
QY 61 APLKGGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQ 120  
DB 61 APLKGGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQ 120  
QY 121 FPGLYFIVCQLQFLVQCNSHSDLTQLLINSKIKKQTLVTVCSGVQSKNIYQNSQFL 180  
DB 121 FPGLYFIVCQLQFLVQCNSHSDLTQLLINSKIKKQTLVTVCSGVQSKNIYQNSQFL 180  
QY 181 LHYLVNSTISVRVDNFOYVDNTFFPLDNVLSVFLYSSD 220  
DB 181 LHYLVNSTISVRVDNFOYVDNTFFPLDNVLSVFLYSSD 220

RESULT 4  
US-09-079-785-19  
Sequence 19, Application US/09079785  
Patent No. 6143869  
GENERAL INFORMATION:  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
APPLICANT: Armitage, Richard J.  
APPLICANT: Gruss, Hans-Jurgen  
TITLE OF INVENTION: No. 6143869el Cytokine That Binds CD30  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1

SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA: US/09/079,785  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA: US/08/225,989  
FILING DATE: 12 APRIL 1994  
APPLICATION NUMBER: US 07/966,775  
FILING DATE: 27-OCT-1992  
CLASSIFICATION:  
PRIOR APPLICATION DATA: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 220 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-079-785-19

Query Match 100.0%; Score 1141; DB 4; Length 220;  
Best Local Similarity 100.0%; Pred. No. 2.le-110;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MQVPGSVASPRWSTPRWSTRSFYLSLTALVCLVAVAILLVVQVKDSTPNTTEK 60  
DB 1 MQVPGSVASPRWSTPRWSTRSFYLSLTALVCLVAVAILLVVQVKDSTPNTTEK 60  
QY 61 APLKGGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQ 120  
DB 61 APLKGGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQ 120  
QY 121 FPGLYFIVCQLQFLVQCNSHSDLTQLLINSKIKKQTLVTVCSGVQSKNIYQNSQFL 180  
DB 121 FPGLYFIVCQLQFLVQCNSHSDLTQLLINSKIKKQTLVTVCSGVQSKNIYQNSQFL 180  
QY 181 LHYLVNSTISVRVDNFOYVDNTFFPLDNVLSVFLYSSD 220  
DB 181 LHYLVNSTISVRVDNFOYVDNTFFPLDNVLSVFLYSSD 220

RESULT 5  
US-08-225-989-6  
Sequence 6, Application US/08225989  
Patent No. 5480981  
GENERAL INFORMATION:  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
APPLICANT: Armitage, Richard J.  
APPLICANT: Gruss, Hans-Jurgen  
TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,989  
FILING DATE: 12 APRIL 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/966,775  
FILING DATE: 27-OCT-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-225-989-6

Query Match 100.0%; Score 1141; DB 1; Length 239;  
Best Local Similarity 100.0%; Pred. No. 2.4e-110;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQVPGSVASPRSTRPWRSTRSRFYLLSTALVCLVAVAILLVVQKDKSTPTTEK 60  
DB 20 MQVPGSVASPRSTRPWRSTRSRFYLLSTALVCLVAVAILLVVQKDKSTPTTEK 79  
QY 61 APLKGGNCSEDLFTCLKSTPKSKSWAYLOVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 120  
DB 80 APLKGGNCSEDLFTCLKSTPKSKSWAYLOVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 139  
QY 121 FPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQTLVTVCEGVSQSKNIYONLSQFL 180  
DB 140 FPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQTLVTVCEGVSQSKNIYONLSQFL 199  
QY 181 LHYLVQNSTISVRVDNQYDNTFTPLDNVLSVFLYSSD 220  
DB 200 LHYLVQNSTISVRVDNQYDNTFTPLDNVLSVFLYSSD 239

RESULT 6

US-08-570-923-6

; Sequence 6, Application us/08570923

; Patent No. 5677430

GENERAL INFORMATION:  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
APPLICANT: Armitage, Richard J.  
APPLICANT: Gruss, Hans-Jurgen  
TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/570,923  
FILING DATE: 12-DEC-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,989  
FILING DATE: 12 APRIL 1994  
APPLICATION NUMBER: US 07/966,775  
FILING DATE: 27-OCT-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-570-923-6

Query Match 100.0%; Score 1141; DB 1; Length 239;  
Best Local Similarity 100.0%; Pred. No. 2.4e-110;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQVPGSVASPRSTRPWRSTRSRFYLLSTALVCLVAVAILLVVQKDKSTPTTEK 60  
DB 20 MQVPGSVASPRSTRPWRSTRSRFYLLSTALVCLVAVAILLVVQKDKSTPTTEK 79  
QY 61 APLKGGNCSEDLFTCLKSTPKSKSWAYLOVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 120  
DB 80 APLKGGNCSEDLFTCLKSTPKSKSWAYLOVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 139  
QY 121 FPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQTLVTVCEGVSQSKNIYONLSQFL 180  
DB 140 FPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQTLVTVCEGVSQSKNIYONLSQFL 199



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;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-079-785-6

Query Match 100.0%; Score 1141; DB 4; Length 239;
Best Local Similarity 100.0%; Pred. No. 2.4e-110; Indels 0; Gaps 0;
Matches 220; Conservative 0; Mismatches 0;

Qy 1 MQVQPGSVASPRWSTRSYFYLSTTALVCLVAVAIILVVLVQKKDSTPNTTEK 60
Db 20 MQVQPGSVASPRWSTRSYFYLSTTALVCLVAVAIILVVLVQKKDSTPNTTEK 79

Qy 61 APLKGGNCSEDLFCTLKSTPSKSWAYLOVSKHLNNTKLSWNEEDGTIHGLIYODGNLIVQ 120
Db 80 APLKGGNCSEDLFCTLKSTPSKSWAYLOVSKHLNNTKLSWNEEDGTIHGLIYODGNLIVQ 139

Qy 121 FPLGLYFIVCOLQFLVQCSNHSVDLTQLLINSKIKKQTLVTVCESGVQSKNIYONLSQFL 180
Db 140 FPLGLYFIVCOLQFLVQCSNHSVDLTQLLINSKIKKQTLVTVCESGVQSKNIYONLSQFL 199

Qy 181 LHLYQVNSTISVRDNFQVVDNTFPLDNVLSVFLYSSSD 220
Db 200 LHLYQVNSTISVRDNFQVVDNTFPLDNVLSVFLYSSSD 239

RESULT 9
US-08-225-989-23
; Sequence 23, Application US/08225989
; Patent No. 5480981
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
```

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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-225-989-23

Query Match 71.4%; Score 814.5; DB 1; Length 215;
Best Local Similarity 70.6%; Pred. No. 1.2e-76;
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

Qy 1 MQVQPGSVASPRWSTRSYFYLSTTAL-VCLVAVAIILVVLVQKKDSTPNTTE 59
Db 1 MHVPAGSVAS-----HLGFTSRSYFYLTTATLALCLVFTVATIMVLVQRTDSIPNSPD 54

Qy 60 KAPLKGNCSEDLFCTLKSTPSKSWAYLOVSKHLNNTKLSWNEEDGTIHGLIYODGNLIV 119
Db 55 NVPLKGGNCSEDLCLILKRAPFKASWAYLQVAKHLNNTKLSWNGDGLHGVYODGNLVI 114

Qy 120 QPFLYFIVCOLQFLVQCSNHSVDLTQLLINSKIKKQTLVTVCESGVQSKNIYONLSQF 179
Db 115 QPFLYFIVCOLQFLVQCPNNSVDLKLLELINKHKKQALVTVCESGMQTKHVYQNLQSF 174

Qy 180 LHLYQVNSTISVRDNFQVVDNTFPLDNVLSVFLYSSSD 220
Db 175 LLDYQVNTTISVNVDTFQYIDTSTFPLENVLISFLYSNSD 215

RESULT 10
US-08-570-923-23
; Sequence 23, Application US/08570923
; Patent No. 5677430
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,923
; FILING DATE: 12-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
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;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 892,459  
;; FILING DATE: 02-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 889,717  
;; FILING DATE: 26-MAY-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Seese, Kathryn A.  
;; REGISTRATION NUMBER: 32,172  
;; REFERENCE/DOCKET NUMBER: 2804-E  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206)587-0430  
;; TELEFAX: (206)233-0644  
;; TELEX: 756822  
;; INFORMATION FOR SEQ ID NO: 23:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 215 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-570-923-23

Query Match 71.4%; Score 814.5; DB 1; Length 215;  
Best Local Similarity 70.6%; Pred. No. 1.2e-76;  
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;  
QY 1 MOVQPGSVASPRWSTPRWSTSRYSFYLLSTAL-VCLVAVAVAILVLVQKDKSTPNTTE 59  
DB 1 MHVPAGSVAS-----HLGTTSRYSFYLLTATLALCLVFTVATIMVLVQRTDSIPNSPD 54  
QY 60 KAPLKGNCSEDLFCTLKSTPSKKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIV 119  
DB 55 NVPLKGGNCSEDLCLILKRAPFKKSWAYLQVAKHLNKTLSWNKDGILHGVRYQDGNLVI 114  
QY 120 QPGLYFIVCOLQFLVQCSNHSVDLTQLLLINSKIKKQTLVTVCSGVQSKNIYQNLISQF 179  
DB 115 QPGLYFIIICQLQFLVQCPNNSVDLKLLELLINKHKKQALVTVCSGMQTKHYQNLISQF 174  
QY 180 LLHYLQVNSTISVRVDFQYDVTNTFPLDNVLSFVLYSSD 220  
DB 175 LLDYLQVNTTISVNVDTFTQYIDTSTFPLENLSIFLYSNSD 215

RESULT 11  
US-08-580-014-23  
; Sequence 23, Application US/08580014  
; Patent No. 5753203  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/580,014  
; FILING DATE: 20-DEC-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989

;; FILING DATE: 12 APRIL 1994  
;; APPLICATION NUMBER: US 07/966,775  
;; FILING DATE: 27-OCT-1992  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 907,224  
;; FILING DATE: 01-JUL-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 899,660  
;; FILING DATE: 15-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 892,459  
;; FILING DATE: 02-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 889,717  
;; FILING DATE: 26-MAY-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Seese, Kathryn A.  
;; REGISTRATION NUMBER: 32,172  
;; REFERENCE/DOCKET NUMBER: 2804-E  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206)587-0430  
;; TELEFAX: (206)233-0644  
;; TELEX: 756822  
;; INFORMATION FOR SEQ ID NO: 23:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 215 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-580-014-23

Query Match 71.4%; Score 814.5; DB 1; Length 215;  
Best Local Similarity 70.6%; Pred. No. 1.2e-76;  
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;  
QY 1 MOVQPGSVASPRWSTPRWSTSRYSFYLLSTAL-VCLVAVAVAILVLVQKDKSTPNTTE 59  
DB 1 MHVPAGSVAS-----HLGTTSRYSFYLLTATLALCLVFTVATIMVLVQRTDSIPNSPD 54  
QY 60 KAPLKGNCSEDLFCTLKSTPSKKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIV 119  
DB 55 NVPLKGGNCSEDLCLILKRAPFKKSWAYLQVAKHLNKTLSWNKDGILHGVRYQDGNLVI 114  
QY 120 QPGLYFIVCOLQFLVQCSNHSVDLTQLLLINSKIKKQTLVTVCSGVQSKNIYQNLISQF 179  
DB 115 QPGLYFIIICQLQFLVQCPNNSVDLKLLELLINKHKKQALVTVCSGMQTKHYQNLISQF 174  
QY 180 LLHYLQVNSTISVRVDFQYDVTNTFPLDNVLSFVLYSSD 220  
DB 175 LLDYLQVNTTISVNVDTFTQYIDTSTFPLENLSIFLYSNSD 215

RESULT 12  
US-09-079-785-23  
; Sequence 23, Application US/09079785  
; Patent No. 6143869  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 6143869el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,785
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-079-785-23

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Query Match 71.4%; Score 814.5; DB 4; Length 215;
Best Local Similarity 70.6%; Pred. No. 1.2e-76;
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

Qy 1 MQVQPGSVASPMRSTRPWRSTSRYSFYLTAL-VCLVAVAILVLVQKDKSTPNTTE 59
Db 1 MHVPAGSVAS-----HLGTTSRYSFYLTALCLCLVFTVATIMVLVQRTDSIPNSPD 54

Qy 60 KAPLKGNCSEDLCTLKSTPSSKSWAYLQVSKHLNNTKLSNEDGTIHLIYODGNLIV 119
Db 55 NVPLKGGNCSEDLICILKRAPPKSWAYLQVAKHLNNTKLSNKGILHGVRYODGNLVI 114

Qy 120 QPGLYFIICQLQFLVQCPNNSVDLKLKLELLINKHKKQALVTVCESGVSKNIYQNLQSF 179
Db 115 QPGLYFIICQLQFLVQCPNNSVDLKLKLELLINKHKKQALVTVCESGMQTKHYVQNLQSF 174

Qy 180 LLHYLQVNSTISVRVDFQYVDNTFPDLNVLVSFLYSSSD 220
Db 175 LLDYLVQNTTISVNDTFQYIDTSTFPLENVLVSFLYSSSD 215

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RESULT 13
US-08-225-989-8
; Sequence 8, Application US/08225989
; Patent No. 5480981
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen

```

```

; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-225-989-8

Query Match 71.4%; Score 814.5; DB 1; Length 234;
Best Local Similarity 70.8%; Pred. No. 1.3e-76;
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

Qy 1 MQVQPGSVASPMRSTRPWRSTSRYSFYLTAL-VCLVAVAILVLVQKDKSTPNTTE 59
Db 20 MHVPAGSVAS-----HLGTTSRYSFYLTALCLCLVFTVATIMVLVQRTDSIPNSPD 73

Qy 60 KAPLKGNCSEDLCTLKSTPSSKSWAYLQVSKHLNNTKLSNEDGTIHLIYODGNLIV 119
Db 74 NVPLKGGNCSEDLICILKRAPPKSWAYLQVAKHLNNTKLSNKGILHGVRYODGNLVI 133

Qy 120 QPGLYFIICQLQFLVQCPNNSVDLKLKLELLINKHKKQALVTVCESGVSKNIYQNLQSF 179
Db 134 QPGLYFIICQLQFLVQCPNNSVDLKLKLELLINKHKKQALVTVCESGMQTKHYVQNLQSF 193

Qy 180 LLHYLQVNSTISVRVDFQYVDNTFPDLNVLVSFLYSSSD 220
Db 194 LLDYLVQNTTISVNDTFQYIDTSTFPLENVLVSFLYSSSD 234

RESULT 14

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US-08-570-923-8  
; Sequence 8, Application US/08570923  
; Patent No. 5677430  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/570,923  
; FILING DATE: 12-DEC-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 234 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-570-923-8

Query Match 71.4%; Score 814.5; DB 1; Length 234;  
Best Local Similarity 70.6%; Pred. No. 1.3e-76;  
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

QY 1 MQVQGSVSPWRSTPWRSTSRYSFYLTAL-VCLWAVAILVLVQKSTPNTTE 59  
Db 20 MHVPAGSVAS-----HLGTSRSFYLTATLALCLVETVATIMLVVQRTDSIPNSPD 73  
QY 60 KAPLKGNCSEDLFCYLKSTPSPKSNAYLQVSKHLNKLWNEDGTHGLIYQDGNLIV 119  
Db 74 NVPLKGCNCEDELLCLIKRAPFKSNAYLQVAKHLNKLWNKDKGLHGVRYQDGNLVI 133

QY 120 QPGLYFTVCOLOFLVQCSNHSVDLTLLINKSKTKOTLVTCESGVQSKNIYONLSQF 179  
Db 134 QPGLYFTVCOLOFLVQCPNNSVDLKLLELLINKHKKALVTVCSGMQTRHYONLSQF 193  
QY 180 LLHYLQVNSTISVRVDFQYVDVDTNFFPLDNVLSVFLYSSSD 220  
Db 194 LLDYLVQVNTTISVNVDTFQYIDTSTFPLENVLSIFLYNSD 234  
RESULT 15  
US-08-580-014-8  
; Sequence 8, Application US/08580014  
; Patent No. 5753203  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/580,014  
; FILING DATE: 20-DEC-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 234 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-580-014-8

Query Match 71.4%; Score 814.5; DB 1; Length 234;  
Best Local Similarity 70.6%; Pred. No. 1.3e-76;

Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

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QY 1  MQVPGSVASPRSTRPWRSTSRSYFYLTAL-VCLWVAIAIILVLVQKKDSTPNTTE 59
Db 20 MHPAGSVAS-----HLGTTSRSYFYLTATLALCLVFTVATIMVLVQRTDSIPNSPD 73
QY 60 KAPLKGNCSEDLFTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHLIYODGNLIV 119
Db 74 NVPLKGCNCSEDLILKRAPFKKSWAYLQVAKHLNNTKLSWNKDGILHGVRYODGNLVI 133
QY 120 OFEGLYFIVCOLQFLVQCSNHSVDLTQLILINSKIKKQTLVTVCESGVQSKNIYQNL SQF 179
Db 134 QPFLYFIICQLQFLVQCPNNSVDLKLLELLINKHKKQALVTVCESGMQTKHYYQNL SQF 193
QY 180 LLHYLQVNSTISVRVDNFQVDTNTPFLDNVLSVFLYSSSD 220
Db 194 LLDYLQVNTTISVNDTFQYIDISTFPLENVLSIFLYSNSD 234

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Search completed: September 5, 2001, 10:23:11  
Job time: 86 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2001, 10:22:39 ; Search time 44.86 Seconds  
(without alignments)  
297.309 Million cell updates/sec

Title: US-09-628-126-19

Perfect score: 1141

Sequence: 1 MQVQGSVSPWRSTRPWS.....DTNFTPLDNLVSLFLYSSD 220

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
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12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1141	100.0	220	14 AAR45006	Sequence encoded b
2	1141	100.0	239	14 AAR45008	Sequence encoded b
3	814.5	71.4	215	14 AAR45007	Sequence encoded b
4	814.5	71.4	234	14 AAR45009	Sequence encoded b
5	742	65.0	143	21 AAB08277	Amino acid sequenc
6	600	52.6	143	21 AAB08276	Amino acid sequenc
7	112	9.8	279	17 AAR88357	Mouse Fas ligand.
8	109	9.6	179	16 AAR79069	Mouse Fas ligand (
9	109	9.6	279	16 AAR79098	Mouse Fas ligand.
10	104	9.1	279	16 AAR77282	Mouse Fas-L protei
11	97	8.5	138	16 AAR79068	Mouse Fas ligand (

12	97	8.5	143	21	AAB08266	Amino acid sequenc
13	95	8.3	137	16	AAR79067	Mouse Fas ligand (
14	92.5	8.1	258	20	AAV04371	Human Fas ligand d
15	91	8.0	179	16	AAR79066	Rat Fas ligand (pa
16	91	8.0	278	16	AAR79095	Rat Fas ligand enc
17	91	8.0	278	20	AAW98069	Rat Fas ligand (Fa
18	91	8.0	278	20	AAW95040	Rat FasL protein.
19	89	7.8	271	20	AAV28596	Fas ligand (FasL)
20	88.5	7.8	309	16	AAR64189	Murine 4-1BB-L pol
21	88.5	7.8	309	18	AAW26656	Murine 4-1BB ligan
22	88.5	7.8	448	21	AAB28694	FC-muAGP-1 (99-291
23	87	7.6	2013	21	AAB18265	Plasmodium falcipa
24	86.5	7.6	268	19	AAW48953	Non-cleavable Fas
25	86	7.5	319	22	AAB87774	Human TR44 amino
26	85	7.4	143	21	AAB08267	Amino acid sequenc
27	85	7.4	281	20	AAV04373	Human Fas ligand d
28	85	7.4	281	21	AAV87576	Human Fas ligand (
29	85	7.4	281	21	AAV87581	Human Fas ligand (
30	85	7.4	291	18	AAW19788	Mouse apoptosis in
31	85	7.4	291	19	AAW36762	Murine TRAIL polyp
32	85	7.4	291	19	AAW44353	Murine AGP-1. Mus
33	85	7.4	426	21	AAB28695	FC-muAGP-1 (120-29
34	84	7.4	265	19	AAW48954	Non-cleavable Fas
35	84	7.4	277	20	AAV04372	Human Fas ligand d
36	84	7.4	281	16	AAV77281	Human Fas-L protei
37	84	7.4	281	16	AAR79097	Human Fas ligand.
38	84	7.4	281	17	AAR98104	Human Fas ligand d
39	84	7.4	281	17	AAR88356	Human Fas ligand.
40	84	7.4	281	18	AAW27143	Human Fas ligand.
41	84	7.4	281	19	AAW75959	Human Fas ligand.
42	84	7.4	281	19	AAW49105	Fas ligand. Mamma
43	84	7.4	281	20	AAV28594	Wild type Fas liga
44	84	7.4	281	20	AAV98071	Human Fas ligand (
45	84	7.4	281	20	AAW95041	Human FasL protein

#### ALIGNMENTS

RESULT 1  
ID AAR45006 standard; Protein; 220 AA.  
XX AAR45006;  
XX AC  
XX 19-JUN-1994 (first entry)  
XX Sequence encoded by a murine CD30-L cDNA clone.  
DE Hodgkin's disease; lymphoma; surface antigen; cytokine;  
KW CD30 ligand; CD30-L; TNF; NGF.  
XX Acomys cahirinus.  
XX Key  
FH Region  
FT Location/Qualifiers  
FT 28..48  
FT /label= transmembrane  
XX WO9324135-A.  
XX 09-DEC-1993.  
XX 25-MAY-1993; 93WO-US04926.  
XX 26-MAY-1992; 92US-0889717.  
PR 02-JUN-1992; 92US-0892459.  
PR 15-JUN-1992; 92US-0899660.  
PR 01-JUL-1992; 92US-0907224.  
PR 27-OCT-1992; 92US-0966775.  
XX (IMMV ) IMMUNEX CORP.  
XX Armitage RJ, Goodwin RG, Smith CA;

```

XX WPI; 1993-405417/50.
DR N-PSDB; AAQ53535.
XX
XX New cytokine, CD30-L, which binds CD30 - used for developing
PT prods. for diagnosis, detection, purifications, research and
PT therapy
XX
XX Claim 15; Figure 3a; 59pp; English.
XX
XX CD30-L is a ligand for CD30, the 120kd surface antigen widely used
CC as a clinical marker for Hodgkin's lymphoma and related haematologic
CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
CC L and other derived prods. can be used for elucidating the roles
CC that CD30 and CD30-L may play in the immune system and for diagnosis
CC and therapy. It can be isolated as follows. A cDNA library prepd. from
CC the murine helper T-cell line 7B9 is screened with a CD30/FC fusion
CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L.
CC This cDNA can then be used as a probe to screen a human PBL cDNA
CC library to obtain cDNA encoding human CD30-L.
XX
XX Sequence 220 AA;
XX
Query Match 100.0%; Score 1141; DB 14; Length 220;
Best Local Similarity 100.0%; Pred. No. 2.2e-108;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQVQPGSVASPWRTSRPWRSTSRSYFYLTALVCLVAVAILLVVQKKDSTPNTTEK 60
Db 1 mqvqpgsvaspwrtsrpwrstsrsyfytalvclvavailvlvqkdkdstpnttek 60
QY 61 APLKGGNCSEDLFTCLKSTPKSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQ 120
Db 61 aplkggncseadlftclkstpskkswaylqvskhlntklswnedgtihlyqdggnliq 120
QY 121 FPGLYFIVCOLQFLVQCSNHSVDLTQLLINSKIKKQTLVTVCESGVQSKNIYQNLSQL 180
Db 121 fpglyfivcolqflvqcsnhsvdltqlllnskikkqtlvtvcsgvqskniyqnlsql 180
QY 181 LHYLVQNSTISVRVDNFQYVDTNFTPLDNVLSVFLYSSSD 220
Db 181 lhylvqnstisvrvdnfyvdtntfpldnvlsvflysssd 220
RESULT 2
AAR45008
ID AAR45008 standard; Protein; 239 AA.
XX
XX AAR45008;
XX
XX 19-JUN-1994 (first entry)
XX
XX Sequence encoded by a murine CD30-L cDNA clone
DE encoding additional N-terminal amino acids.
XX
XX Hodgkin's disease; lymphoma; surface antigen; cytokine;
KW CD30 ligand; CD30-L; TNF; NGF.
XX
XX Acomys cahirinus.
XX
XX Key Location/Qualifiers
FT Region 47..67
FT /label= Transmembrane
XX
XX W09324135-A.
XX
XX 09-DEC-1993.
XX
XX 25-MAY-1993; 93WO-US04926.
XX
XX 26-MAY-1992; 92US-0889717.
PR 02-JUN-1992; 92US-0892459.

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PR 15-JUN-1992; 92US-0899660.
PR 01-JUL-1992; 92US-0907224.
PR 27-OCT-1992; 92US-0966775.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Armitage RJ, Goodwin RG, Smith CA;
PI WPI; 1993-405417/50.
DR N-PSDB; AAQ53537.
XX
XX New cytokine, CD30-L, which binds CD30 - used for developing
PT prods. for diagnosis, detection, purifications, research and
PT therapy
XX
XX Claim 15; Figure 6a; 59pp; English.
XX
XX CD30-L is a ligand for CD30, the 120kd surface antigen widely used
CC as a clinical marker for Hodgkin's lymphoma and related haematologic
CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
CC L and other derived prods. can be used for elucidating the roles
CC that CD30 and CD30-L may play in the immune system and for diagnosis
CC and therapy. It can be isolated as follows. A cDNA library prepd. from
CC the murine helper T-cell line 7B9 is screened with a CD30/FC fusion
CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L
CC (AAQ53535). This cDNA can then be used as a probe to screen a human PBL
CC cDNA library to obtain cDNA encoding human CD30-L (AAQ53536). An
CC anchored PCR technique was employed to isolate CD30-L human and murine
CC clones containing an additional 19 N-terminal amino acid sequence
CC (AAQ53537, AAQ53538).
XX
XX Sequence 239 AA;
XX
Query Match 100.0%; Score 1141; DB 14; Length 239;
Best Local Similarity 100.0%; Pred. No. 2.4e-108;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQVQPGSVASPWRTSRPWRSTSRSYFYLTALVCLVAVAILLVVQKKDSTPNTTEK 60
Db 20 mqvqpgsvaspwrtsrpwrstsrsyfytalvclvavailvlvqkdkdstpnttek 79
QY 61 APLKGGNCSEDLFTCLKSTPKSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQ 120
Db 80 aplkggncsedlftclkstpskkswaylqvskhlntklswnedgtihlyqdggnliq 139
QY 121 FPGLYFIVCOLQFLVQCSNHSVDLTQLLINSKIKKQTLVTVCESGVQSKNIYQNLSQL 180
Db 140 fpglyfivcolqflvqcsnhsvdltqlllnskikkqtlvtvcsgvqskniyqnlsql 199
QY 181 LHYLVQNSTISVRVDNFQYVDTNFTPLDNVLSVFLYSSSD 220
Db 200 lhylvqnstisvrvdnfyvdtntfpldnvlsvflysssd 239
RESULT 3
AAR45007
ID AAR45007 standard; Protein; 215 AA.
XX
XX AAR45007;
XX
XX 19-JUN-1994 (first entry)
XX
XX Sequence encoded by a human CD30-L cDNA clone.
DE
XX Hodgkin's disease; lymphoma; surface antigen; cytokine;
KW CD30 ligand; CD30-L; TNF; NGF.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Region 22..43
FT /label= transmembrane

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XX PN WO9324135-A.
XX PD 09-DEC-1993.
XX PF 25-MAY-1993; 93WO-US04926.
XX PR 26-MAY-1992; 92US-0889717.
XX PR 02-JUN-1992; 92US-0892459.
XX PR 15-JUN-1992; 92US-0899660.
XX PR 01-JUL-1992; 92US-0907224.
XX PR 27-OCT-1992; 92US-0966775.
XX PA (IMMV ) IMMUNEX CORP.
XX PI Armitage RJ, Goodwin RG, Smith CA;
XX DR WPI: 1993-405417/50.
XX DR N-PSDB; AAQ53536.
XX PT New cytokine, CD30-L, which binds CD30 - used for developing
XX PT prods. for diagnosis, detection, purifications, research and
XX PT therapy
XX PS Claim 15; Figure 5a; 59pp; English.
XX CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
XX CC as a clinical marker for Hodgkin's lymphoma and related haematologic
XX CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
XX CC L and other derived prods. can be used for elucidating the roles
XX CC that CD30 and CD30-L may play in the immune system and for diagnosis
XX CC the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion
XX CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L.
XX CC This cDNA can then be used as a probe to screen a human PBL cDNA
XX CC library to obtain cDNA encoding human CD30-L.
XX SQ Sequence 215 AA;

Query Match 71.4%; Score 814.5; DB 14; Length 215;
Best Local Similarity 70.6%; Pred. No. 3.9e-75;
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

Qy 1 MQVPGSVASPMWRSTRPWRSTRSRYSFYLTSTAL-VCLVAVAVAILLVQVKDSTPNTE 59
Db 1 mhvpagsvas-----hlgtsrsyfytatlalclvftvatimlvvqrtdsipnsdpd 54

Qy 60 KAPLKGNCSEDLFCTLKSTPPSKSWAYLQVSKHLNNTKLSWNEGTGTHGLIYQDGNLIV 119
Db 55 nvplkgncsedllcilkrapfkkswaylqvakhlnktklswnkdgilhgvyrgdgnlvi 114

Qy 120 QPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQTLVTVCESGVQSKNIYQNLISQF 179
Db 115 qfpglyfiicqlqflvqcpnnsvdlllellinkhkkqaltvcesgmqtkhvyqnlisqf 174

Qy 180 LLHYLQVNSTISVRVDFQYVDNTFPPLDNVLSVFLYSSSD 220
Db 175 lldylqvnstisvrndfgydtstfplenvlsiflynsnd 215

RESULT 4
AAR45009
ID AAR45009 standard; Protein; 234 AA.
XX AC AAR45009;
XX DT 19-JUN-1994 (first entry)
XX DE Sequence encoded by a human CD30-L cDNA clone
XX DE encoding additional N-terminal amino acids.
XX KW Hodgkin's disease; lymphoma; surface antigen; cytokine;

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KW CD30 ligand; CD30-L; TNF; NGF.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Region 41..62
XX FT /label= Transmembrane
XX XX WO9324135-A.
XX XX 09-DEC-1993.
XX XX 25-MAY-1993; 93WO-US04926.
XX XX 26-MAY-1992; 92US-0889717.
XX XX 02-JUN-1992; 92US-0892459.
XX XX 15-JUN-1992; 92US-0899660.
XX XX 01-JUL-1992; 92US-0907224.
XX XX 27-OCT-1992; 92US-0966775.
XX PA (IMMV ) IMMUNEX CORP.
XX PI Armitage RJ, Goodwin RG, Smith CA;
XX XX WPI: 1993-405417/50.
XX XX N-PSDB; AAQ53538.
XX XX New cytokine, CD30-L, which binds CD30 - used for developing
XX XX prods. for diagnosis, detection, purifications, research and
XX XX therapy
XX XX Claim 15; Figure 7a; 59pp; English.
XX XX CD30-L is a ligand for CD30, the 120kd surface antigen widely used
XX XX as a clinical marker for Hodgkin's lymphoma and related haematologic
XX XX malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
XX XX L and other derived prods. can be used for elucidating the roles
XX XX that CD30 and CD30-L may play in the immune system and for diagnosis
XX XX and therapy. It can be isolated as follows. A cDNA library prepd. from
XX XX the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion
XX XX protein labelled with (125)I to obtain cDNA encoding murine CD30-L
XX XX (AAQ53535). This cDNA can then be used as a probe to screen a human PBL
XX XX cDNA library to obtain cDNA encoding human CD30-L (AAQ53536). An
XX XX anchored PCR technique was employed to isolate CD30-L human and murine
XX XX clones containing an additional 19 N-terminal amino acid sequence
XX XX (AAQ53537, AAQ53538).
XX SQ Sequence 234 AA;

Query Match 71.4%; Score 814.5; DB 14; Length 234;
Best Local Similarity 70.6%; Pred. No. 4.4e-75;
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

Qy 1 MQVPGSVASPMWRSTRPWRSTRSRYSFYLTSTAL-VCLVAVAVAILLVQVKDSTPNTE 59
Db 20 mhvpagsvas-----hlgtsrsyfytatlalclvftvatimlvvqrtdsipnsdpd 73

Qy 60 KAPLKGNCSEDLFCTLKSTPPSKSWAYLQVSKHLNNTKLSWNEGTGTHGLIYQDGNLIV 119
Db 74 nvplkgncsedllcilkrapfkkswaylqvakhlnktklswnkdgilhgvyrgdgnlvi 133

Qy 120 QPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQTLVTVCESGVQSKNIYQNLISQF 179
Db 134 qfpglyfiicqlqflvqcpnnsvdlllellinkhkkqaltvcesgmqtkhvyqnlisqf 193

Qy 180 LLHYLQVNSTISVRVDFQYVDNTFPPLDNVLSVFLYSSSD 220
Db 194 lldylqvnstisvrndfgydtstfplenvlsiflynsnd 234

RESULT 5
AAB08277

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ID AAB08277 standard; Protein; 143 AA.  
 AC AAB08277;  
 DT  
 DE 04-DEC-2000 (first entry)  
 DE Amino acid sequence of a mouse TNF ligand CD30L.  
 KW AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;  
 KW type II transmembrane protein; B cell stimulatory factor;  
 KW inflammatory disorder; immune disorder; rheumatoid arthritis;  
 KW lupus and graft versus host disease.  
 XX  
 OS Mus sp.  
 XX  
 PN WO200047740-A2.  
 XX  
 PD 17-AUG-2000.  
 XX  
 PF 11-FEB-2000; 2000WO-US03653.  
 XX  
 PR 12-FEB-1999; 99US-0119906.  
 PR 18-NOV-1999; 99US-0166271.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Boyle WJ, Hsu H;  
 XX  
 DR WPI; 2000-558217/51.  
 XX  
 PT Novel polypeptides comprising tumour necrosis factor ligand family  
 PT proteins, useful for treating inflammatory and immune disorders, e.g.  
 PT rheumatoid arthritis -  
 XX  
 PS Claim 14; Fig 9; 71pp; English.  
 XX  
 CC AAB08265-83 represent tumour necrosis factor (TNF) ligands. The  
 CC specification describes an AGP-3 polypeptide, which is TNF ligand  
 CC family member. AGP-3 is a type II transmembrane protein, and is a  
 CC potent B cell stimulatory factor. Expression of AGP-3 correlates to  
 CC increases in the number of B cells and immunoglobulins produced.  
 CC AGP-3 proteins, antibodies, and nucleic acids may be used to treat  
 CC inflammatory and immune disorders, e.g. rheumatoid arthritis,  
 CC Crohn's disease, lupus and graft versus host disease. The nucleic  
 CC acids may be used to regulate the expression of an AGP-3 related  
 CC protein. The AGP-3 proteins, antibodies and nucleic acids are also  
 CC useful for the detection of AGP-3 agonists, antagonists and  
 CC characterizing interactions with AGP-3 related proteins.  
 XX  
 SQ Sequence 143 AA;  
 Query Match 65.0%; Score 742; DB 21; Length 143;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-68;  
 Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 78 STPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQFPGLYFTVCOLQFLVQC 137  
 Db 1 stpskswaylqvskhlntklswnedgtihgliyqdglnlviqfpglyftvcqlqflvqc 60  
 Qy 138 SNHSVDLTQLLINSKIKKQTLVTVCESGVQSKNIYONLSQFLHLHYLVQNSTISVRVDNF 197  
 Db 61 snhsvdltqlllnskkikktlvtvcsgvqskniygnlsqflhlhylvqnstisvrvdnf 120  
 Qy 198 QYVDNTFPLDNVLSVFLYSSSD 220  
 Db 121 qyvdntfpldnvlsflysssd 143  
 RESULT 6  
 AAB08276  
 ID AAB08276 standard; Protein; 143 AA.  
 XX

AC AAB08276;  
 XX  
 DT 04-DEC-2000 (first entry)  
 XX  
 DE Amino acid sequence of a human TNF ligand CD30L.  
 XX  
 KW AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;  
 KW type II transmembrane protein; B cell stimulatory factor;  
 KW inflammatory disorder; immune disorder; rheumatoid arthritis;  
 KW lupus and graft versus host disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200047740-A2.  
 XX  
 PD 17-AUG-2000.  
 XX  
 PF 11-FEB-2000; 2000WO-US03653.  
 XX  
 PR 12-FEB-1999; 99US-0119906.  
 PR 18-NOV-1999; 99US-0166271.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Boyle WJ, Hsu H;  
 XX  
 DR WPI; 2000-558217/51.  
 XX  
 PT Novel polypeptides comprising tumour necrosis factor ligand family  
 PT proteins, useful for treating inflammatory and immune disorders, e.g.  
 PT rheumatoid arthritis -  
 XX  
 PS Claim 14; Fig 9; 71pp; English.  
 XX  
 CC AAB08265-83 represent tumour necrosis factor (TNF) ligands. The  
 CC specification describes an AGP-3 polypeptide, which is TNF ligand  
 CC family member. AGP-3 is a type II transmembrane protein, and is a  
 CC potent B cell stimulatory factor. Expression of AGP-3 correlates to  
 CC increases in the number of B cells and immunoglobulins produced.  
 CC AGP-3 proteins, antibodies, and nucleic acids may be used to treat  
 CC inflammatory and immune disorders, e.g. rheumatoid arthritis,  
 CC Crohn's disease, lupus and graft versus host disease. The nucleic  
 CC acids may be used to regulate the expression of an AGP-3 related  
 CC protein. The AGP-3 proteins, antibodies and nucleic acids are also  
 CC useful for the detection of AGP-3 agonists, antagonists and  
 CC characterizing interactions with AGP-3 related proteins.  
 XX  
 SQ Sequence 143 AA;  
 Query Match 52.6%; Score 600; DB 21; Length 143;  
 Best Local Similarity 77.3%; Pred. No. 1.6e-53;  
 Matches 109; Conservative 19; Mismatches 13; Indels 0; Gaps 0;  
 Qy 80 PSKSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQFPGLYFTVCOLQFLVQC 139  
 Db 3 pfkkswaylqvskhlntklswnkdglhwryqdglnlviqfpglyftvcqlqflvqc 62  
 Qy 140 HSDVLTQLLINSKIKKQTLVTVCESGVQSKNIYONLSQFLHLHYLVQNSTISVRVDNF 199  
 Db 63 nsvalklellinkhikgalvtvcsgmqtkhvyqnsqflldylqvmntisvndtfg 122  
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 Db 123 idtstfpldnvlsflysssd 143  
 RESULT 7  
 AAB08357  
 ID AAB08357 standard; Protein; 279 AA.  
 XX  
 AC AAB08357;  
 XX

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XX Mus musculus.
XX OS
XX PN W09513293-A1.
XX PD 18-MAY-1995.
XX PF 10-NOV-1994; 94WO-JP01899.
XX PR 18-OCT-1994; 94JP-0278378.
XX PR 10-NOV-1993; 93JP-0305975.
XX PR 13-DEC-1993; 93JP-0342526.
XX PR 18-MAR-1994; 94JP-0074344.
XX PR 08-JUL-1994; 94JP-0180955.
XX PR 07-SEP-1994; 94JP-0239363.
XX
XX (MOCH ) MOCHIDA PHARM CO LTD.
XX PA (OSAB-) OSAKA BIOSCIENCE INST.
XX
XX Nagata S, Nakamura N, Suda T, Takahashi T;
XX
XX WPI: 1995-194031/25.
XX DR N-PSDB; AAQ99498.
XX
XX Peptide which binds to Fas antigen, and antibody reactive with it
XX for treatment and diagnosis of viral or auto:immune diseases
XX
XX Claim 11; Page 222-224; 300pp; Japanese.
XX
XX Fas ligands or active fragments able to induce apoptosis in cells
XX which express the Fas cell surface antigen are claimed. The
XX CC proteins are isolated from human, rat and mouse sources. The present
XX CC sequence represents part of the mouse Fas ligand.
XX
XX Sequence 179 AA;
XX
XX
XX Query Match 9.6%; Score 109; DB 16; Length 179;
XX Best Local Similarity 26.2%; Pred. No. 0.0024;
XX Matches 37; Conservative 28; Mismatches 46; Indels 30; Gaps
XX
QY 78 STPSKK----SWAYLQVSKHLNNTKLSWNEP-GT--IHGLIYQDGNLIVQFGLYFIVCQ 13
Db 33 stpskkeprsvahitgnphrsiprlewedtygtalisgvkykkgglvinetglyfvysk 92
QY 131 LQFLVQ-CSNHSVDLTQLLNSK-----IKKQTLVTVCESG-----VQ 16
Db 93 vyfgrscnqplnhkvymr-nskypedlvimeekrinycttgqiwahssylgavfnlts 15
QY 169 SKNIYONLSQFLHYLVQNST 189
Db 152 adhlyvnisqlslinfeeskt 172
XX
XX RESULT 9
XX AAR79098
XX ID AAR79098 standard; Protein: 279 AA.
XX AC AAR79098;
XX
XX 21-FEB-1996 (first entry)
XX
XX Mouse Fas ligand.
XX
XX Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;
XX KW Fas cell surface antigen; Fas-L; mouse.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX FT Region 25..78
XX FT /label= proline-rich
XX FT Domain 79..100

```







```

PA (OSAB-) OSAKA BIOSCIENCE INST.
XX
XX Nagata S, Tanaka M;
XX
XX WPI: 1999-229531/19.
DR N-PSDB: AAX33116.
XX
XX Protease-resistant Fas ligand derivatives used for prevention of,
XX e.g. cancer
XX
XX Claim 4; Page 46-47; 60pp; Japanese.
XX
XX The present sequence is a protease-resistant Fas ligand derivative
XX in which a region of human Fas ligand which is susceptible to protease
XX attack has been deleted. The present invention also describes apoptosis
XX modulators containing soluble Fas ligand. The modification in the Fas
XX ligand renders it resistant to the action of proteases such as the
XX metalloproteinase which in vivo cleaves the active membrane-bound Fas
XX ligand (which is active as an apoptosis inducer). The Fas ligand can be
XX used for the prevention and treatment of diseases such as cancer, viral
XX infection and autoimmune disease, e.g. by introduction of DNA encoding
XX the modified Fas ligand into effector cells using a suitable gene
XX therapy vector.
XX
XX Sequence 258 AA;
XX
Query Match 8.1%; Score 92.5; DB 20; Length 258;
Best Local Similarity 21.0%; Pred. No. 0.19;
Matches 42; Conservative 32; Mismatches 53; Indels 73; Gaps 9;
QY 34 VCLVVAVAIILVLV-----QKXDSTPTTEKAPLKGNGCSEDLFCTLKSTPS 81
DB 81 lcllvmfmlvalvglgmqlfhlqkepsp-----pe 116
QY 82 KKSW---AYLQVSKHLNNTKLSWNEDGTI---HGLIYQDGNLIVQFPGLYFVQCQLQFLV 135
DB 117 kkelrkvahitgksnsrsmplewedtygillsgvkkkgglvinetglyfvyskvyfgr 176
QY 136 Q-CSN----HSVDLTQLLINSK-----TKQTLVTVVCSG-----VQS 169
DB 177 qscnnlplshkv-----ymrnskyppqdlvmmegkmsycttgqmwarsylgavfnltsa 231
QY 170 KNIVQNLSQFLHLVQVNST 189
DB 232 dhlyvnvselnvnfeesqt 251
RESULT 15
ID AAR79066
XX AAR79066 standard; Protein; 179 AA.
XX
XX AAR79066;
XX
XX 22-FEB-1996 (first entry)
XX
XX Rat Fas ligand (partial sequence).
DE
XX
XX Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;
KW Fas cell surface antigen; Fas-L; rat.
XX
XX Rattus rattus.
OS
XX
XX W09513293-AL.
PN
XX
XX 18-MAY-1995.
XX
XX 10-NOV-1994; 94WO-JP01899.
XX
XX 18-OCT-1994; 94JP-0278378.
PR
XX 10-NOV-1993; 93JP-0305975.
PR
XX 13-DEC-1993; 93JP-0342526.
PR
XX 18-MAR-1994; 94JP-0074344.

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PR 08-JUL-1994; 94JP-0180955.
PR 07-SEP-1994; 94JP-0239363.
XX
XX (MOCH ) MOCHIDA PHARM CO LTD.
PA (OSAB-) OSAKA BIOSCIENCE INST.
XX
XX Nagata S, Nakamura N, Suda T, Takahashi T;
PI
XX WPI; 1995-194031/25.
DR N-PSDB; AAQ99495.
XX
PT Peptide which binds to Fas antigen, and antibody reactive with it
PT for treatment and diagnosis of viral or auto-immune diseases
XX
PS Claim 7; Page 215-216; 300pp; Japanese.
XX
CC Fas ligands or active fragments able to induce apoptosis in cells
CC which express the Fas cell surface antigen are claimed. The
CC proteins are isolated from human, rat and mouse sources. The present
CC sequence represents part of the rat Fas ligand.
XX
SQ Sequence 179 AA;

Query Match 8.0%; Score 91; DB 16; Length 179;
Best Local Similarity 24.2%; Pred. NO. 0.16;
Matches 37; Conservative 24; Mismatches 52; Indels 40; Gaps 7;

QY 78 SPPSK----KSWAYLQVSKHLNNTKLSWNEG-GT--IHGLIYQDGNLIVQPGLYFIVCQ 130
   ||||:  :| |:  :  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :
Db 33 stpsetkkprsvahitgnprsrspilewedtygtalisgvykkgglvineaglyfvysk 92
   :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :
QY 131 LQFLVQCSN-----HSV-----DLTLQLLINSKIKKQTLVTVCESGVQSKNIYONL 176
   :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :
Db 93 vyfrrgscnsqplshkvymrnfkypgdvlvm-----eekklnycttg----- 134
   :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :
QY 177 SQFLHLYQVNSTISVRVDNFQYVDNTEPLDN 209
   | |  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :
Db 135 -qlwahssylgavfnltvadhlvynisqisln 166

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Search completed: September 5, 2001, 10:22:39  
 Job time: 54 sec

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1094	97.9	234	4	O43404		O43404 homo sapien
2	100	8.9	169	11	Q9WY90		Q9WY90 hormota mon
3	94.5	8.5	234	6	Q9TTJ3		Q9ttj3 equus cabal
4	93.5	8.4	547	14	Q98269		Q98269 molluscum c
5	93	8.3	217	11	Q9ER66		Q9erg6 peromyscus
6	92	8.2	280	6	Q9WYL6		Q9myl6 macaca neme
7	89.5	8.0	896	10	Q9M9B0		Q9m9b0 arabidopsis
8	88	7.9	1109	5	Q9GYH7		Q9gyh7 caenorhabdi
9	87.5	7.8	813	4	Q9Y4N0		Q9y4n0 homo sapien
10	87.5	7.8	1003	4	Q9P207		Q9p207 homo sapien
11	85	7.6	761	3	Q9UVJ1		Q9uvj1 candida alb
12	84.5	7.6	232	4	Q9UIV3		Q9uiv3 homo sapien
13	83.5	7.5	431	10	Q9LIF0		Q9lif0 arabidopsis
14	83	7.4	372	14	Q96717		Q96717 chlorella v
15	83	7.4	636	2	Q56619		Q56619 vibrio chol
16	83	7.4	636	2	Q34235		Q34235 vibrio chol
17	83	7.4	636	2	Q87139		Q87139 vibrio chol
18	83	7.4	640	8	Q9GEV6		Q9gev6 grammadenia
19	82.5	7.4	225	13	Q91B42		Q91b42 paralichthy

Db 80 GNCSEDLICILKRAPFKSWAYLQVAKHLNKTLSNKGILHGVYQDGNLVQIPGLY 139  
Qy 121 FTICOLQFLVQCPNNSVDLKLLELLINKHKKOALVTVCSGMDTKHYQNLQFLDYLO 180  
Db 140 FTICOLQFLVQCPNNSVDLKLLELLINKHKKOALVTVCSGMDTKHYQNLQFLDYLO 199  
Qy 181 VNTTISVNDYTFQYIDTSTFPLENVLISFLXSNSD 215  
Db 200 VNTTISVNDYTFQYIDTSTFPLENVLISFLXSNSD 234  
RESULT 2  
ID Q9WV90 PRELIMINARY; PRT; 169 AA.  
AC Q9WV90;  
DT 01-NOV-1999 (TReMBLrel. 12, Created)  
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
DE FAS LIGAND (FRAGMENT).  
OS Marmota monax (Woodchuck).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;  
OC Marmota.  
OX NCBI\_TaxID=9995;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=HEALTHY LIVER;  
RA Hodgson P.D., Grant M.D., Michalak T.I.;  
RT "Perforin and Fas/Fas ligand-mediated cytotoxicity in acute and  
chronic woodchuck viral hepatitis.",  
RL Clin. Exp. Immunol. 0:0-0(1999).  
DR EMBL; AF152368; AAD38387.1; -  
DR InterPro; IPR000478; -  
DR Pfam; PF00229; TNF\_1; -  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
DR SMART; SM00207; TNF; 1.  
FT NON\_TER 1  
FT NON\_TER 169  
SQ SEQUENCE 169 AA; 19274 MW; FDE395B014717B6B CRC64;

Query Match 8.9%; Score 100; DB 11; Length 169;  
Best Local Similarity 24.6%; Pred. No. 0.024;  
Matches 32; Conservative 23; Mismatches 45; Indels 30; Gaps 5;  
Qy 71 LKRAPFKSWAYLQVAKHLNKTLSNKGILHGVYQDGNLVQIPGLYFICQLQ 127  
Db 40 LRRA-----AHLTGKPNRSRSPLEWDTYGLISLGVYQKGGVLNDTGLYFYVSKY 93  
Qy 128 FLVQ-CPNNSVDLKLLELLINKH-----IKQALVTVCSGM-----QTKH 166  
Db 94 FRGSCNNQPLSHKYVYKNSKYQDVLVMEGKMNYCTTGOMWARSYLGAVNFNFTSNDH 153  
Qy 167 VYQNLQFL 176  
Db 154 LYVNVSELSL 163

RESULT 3  
ID Q9TJ3 PRELIMINARY; PRT; 234 AA.  
AC Q9TJ3;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
DE TUMOR NECROSIS FACTOR-ALPHA.  
GN TNFA.  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=THOROUGHRED; TISSUE=ARTERIAL ENDOTHELIUM;  
RA Ishida N., Sato F., Hasegawa T.;  
RT "Molecular cloning of equine tumor necrosis factor-alpha mRNA";  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB035735; BAA88349.1; -  
DR HSSP; P01375; 4TSV.  
DR InterPro; IPR000478; -  
DR Pfam; PF00229; TNF\_1; -  
DR PRINTS; PR01234; TNECROSISFCT.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
DR SMART; SM00207; TNF; 1.  
SQ SEQUENCE 234 AA; 25430 MW; 2384D4950A21F377 CRC64;

Query Match 8.5%; Score 94.5; DB 6; Length 234;  
Best Local Similarity 24.7%; Pred. No. 0.12;  
Matches 48; Conservative 33; Mismatches 88; Indels 25; Gaps 8;  
Qy 18 SYFLTTATLALCLVFTVATIMVLVWVORTSDIPNSPDVPLKGCNSEDLLCILKRAPFK 77  
Db 37 SFLLVAGATTFLCLLH----FGVIGPOREEQLPNAFOSI-----NPLAQLRSSRTPSD 87  
Qy 78 KSWAYLQVAKHLNKTLSW---NKDGIL-HGVRYQDGNLVQIPGLYFICQLQFLVQ-C 132  
Db 88 KPAHV-VANPOAEGQLWLSGRANALLANGVKLTDLQVPLDGLYLYISQVLFKGGC 146  
Qy 133 PNNSVDL--KLELLINKHKKQALVTVCSGMQT-----KHVQNLSOFLDYLOVN 182  
Db 147 PSTHVLTHTRISLAVSPSKVNLSSAISKLANTESEQAQAKPWEPYILGGVFOLEKG 206  
Qy 183 TTISVNVDTFYID 196  
Db 207 DQLSAEINQPNYLD 220

RESULT 4  
ID Q98269 PRELIMINARY; PRT; 547 AA.  
AC Q98269;  
DT 01-FEB-1997 (TReMBLrel. 02, Created)  
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)  
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
DE MC102L.  
GN MC102L.  
OS Molluscum contagiosum virus subtype 1 (MCV1).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Molluscipoxvirus.  
OX NCBI\_TaxID=10280;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96325459; PubMed=8670425;  
RA Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,  
RA Moss B.;  
RT "Genome sequence of a human tumorigenic poxvirus: prediction of  
specific host response-evasion genes";  
RL Science 273:813-816(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,  
RA Moss B.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U60315; AAC55230.1; -  
SQ SEQUENCE 547 AA; 60513 MW; 6A0C621DCF4B21AA CRC64;

Query Match 8.4%; Score 93.5; DB 14; Length 547;  
Best Local Similarity 24.8%; Pred. No. 0.41;  
Matches 51; Conservative 25; Mismatches 69; Indels 61; Gaps 12;  
Qy 3 VPAG-SVASH-----LGTTSRSYFLTT---ATLALCLVFTVATIMVLVQRT-----DS 48

Query Match	8.34;	Score 93;	DB 11;	Length 217;
Best Local Similarity	24.56;	Pred. No. 0.16;		
Matches	49;	Conservative	31;	Mismatches 84; Indels 36; Gaps 9;
QY	18	SYFVLTTATLALCVETVATIWLVQRTSDIPNSPDNVPLKGGNCSEDLILCILKRAPFK	77	
Db	29	SFLLVAGATTIFCLL-----NGCVIGPQREEKFPN---NLPIIGSMAQTLTLRSSQNSSD	81	
QY	78	KSWAYLOVAKHLNKTKLW---NKDGIL-HGVRYODGNLVTFQPGLYFIICOLQFLVQ-C	132	
Db	82	KPAHV-VANHQVDBOLEWLSRRANALLANGMDLNOLVLPADGLYVYSQVLEKGGCC	140	
QY	133	PNN-----SVDLKLELLINKHKKQALVTVC-----ESGMOTKHVVYQNLSQFLL	176	
Db	141	SNYVLLTHTVSRFAVSIEDKVNLL-----SAIKSPCKETPEGESELPWYEPYILGGV	193	
QY	177	DYLOVNTTISVNDVTFQYID	196	
Db	194	FQLEKGDRLSAEVNLPKYLD	213	
RESULT	6			
Q9MYL6		PRELIMINARY;	PRT;	280 AA.
ID	Q9MYL6			
AC	Q9MYL6;			
DT	01-OCT-2000 (TrEMBLrel. 15, Created)			
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)			
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)			
DE	FAS LIGAND.			
GN	PT-FASL OR CM-FASL OR RM-FASL.			
OS	Macaca nemestrina (pig-tailed macaque),			

```

RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN-BRISTOL N2;
RA      Latreille P.;
RT      "The sequence of C. elegans cosmid F49E7."
RL      Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.

```

Qy	27	LALCVETVATIMVLVQVORTSDISPNSDNNVPLKGGNGCEDLLCILKRAPFKKNWAYLQVA	86
Db	461	LALCSADSAVA-FPVLTHSTRNGLPDHTDPE-----DNEIVCFLK-----VQIA	502
Qy	87	KLHNKTKLSNNKGDLHGVRVYQDGNLVFIQFPGLYFIIICQLQFLVQCPNNSVDLKLLELIN	146
Db	503	EAIN-----LQDNLMQAQLQETMRCVCF-----DNTCRKLLASTA	539
Qy	147	KHKKQ---ALVTVCESGMQT--KHVYQNLSQFLDYLQVN--TTISVN-----	188

```

RT   the adenylate cyclase gene which complements CfrI mutant as well as
RT   six other genes including homologs of CHS6 and SAPI85.*;
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
DR   ENBL; AJ250310; CAB59913.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE      761 AA;  87454 MW;  45B3AF011E57DD0E CRC64;

Query Match          7.6%; Score 85; DB 3; Length 761;
Best Local Similarity 24.7%; Pred. No. 4.2;
Matches 38; Conservative 26; Mismatches 50.; Indels 40; Gaps

Qy    65 EDLLCILKRAPFKSWAYLOVAKHLN--KTKLSNNKDGIIL----HGVRYQDGNLVIOQP 117
      |||:::||||:::||||:::||||:::||||:::||||:::||||:::
Db    551 EDLRITLM-----ITIANSNQERSALEWEMIGLLGSVKINLRDSISSIVTSII 599

Qy    118 GL-----YFIICQL-----QFLVCPNNNSVDLKLELLINKHKIKQAOLVTVCESGMOTK 165
      |||||:::||||:::||||:::||||:::||||:::||||:::||||:::
Db    600 GKNVOGEFDFSTVOLLEIYDEIFDLDCPGYMNDYNGKFESNKLIILRVSSKKMCDS----- 654

Qy    166 HYNQNLSQ---FLLDY---LQVNNTTISNVDTFOYI 195
      ::::|||:::||||:::||||:::||||:::||||:::||||:::
Db    655 -LVRSLEGEYFKLDFVLLAIKLISWNVRWIQIV 687

RESULT 12
Q9UIV3 PRELIMINARY; PRT; 232 AA.
AC Q9UIV3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE TUMOR NECROSIS FACTOR.
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OS   Homo sapiens (human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93272029; PubMed=8499947;
RA   Iris F., Bougueleret L., Prieur S., Caterina D., Primas G., Perrot V.,
RA   Jurka J., Rodriguez-Tome P., Clavierie J., Cohen D., Dausset J.;
RT   "dense Alu clustering and a potential new member of the NF kappa B
RT   family within a 90 kilobase HLA class III segment.";
RL   Nat. Genet. 3:137-145(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96215741; PubMed=8629302;
RA   Utans U., Quist W.C., McManus B.M., Wilson J.E., Arceci R.J.,
RA   Wallace A.F., Russell M.E.;
RT   "Allograft inflammatory factory-1. A cytokine-responsive macrophage
RT   molecule expressed in transplanted human hearts.";
RL   Transplantation 61:1387-1392(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96006565; PubMed=7590964;
RA   Holzinger I., de Baey A., Messer G., Kick G., Zwierzina H.,
RA   Weiss E.H.;
RT   "Cloning and genomic characterization of LSL1: a new gene in the human
RT   TNF region.";
RL   Immunogenetics 42:315-322(1995).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93208881; PubMed=7916655;
RA   Browning J.L., Ngam-ek A., Lawton P., DeMarinis J., Tizard R.,
RA   Chow E.P., Hession C., O'Brine-Greco B., Foley S.F., Ware C.F.;
RT   "Lymphotoxin beta, a novel member of the TNF family that forms a
RT   heteromeric complex with lymphotoxin on the cell surface.";
RL   Cell 72:847-856(1993).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86016093; PubMed=2995927;

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RESULT 14
Q96717          PRELIMINARY;      PRT;      372 AA.
ID Q96717;
AC Q96717;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE DNA ADENINE METHYLTRANSFERASE.
GN M.CVISI.
OS Chlorella virus SC-1A.
OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phycodnavirus.
OX NCBI_TaxID=51374;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97341065; PubMed=9197539;
RA Qie Q., Zhang Y., Nelson M., Ropp S., Burbank D.E., Etten J.L.;
RT "Chlorella virus SC-1A encodes at least five functional and one
RT nonfunctional DNA methyltransferases.";
RL Gene 190:237-244(1997).
DR EMBL; U65736; AAC57943.1; -.
DR HSSP; P14385; IAQJ.
DR REBASE; 3013; M.Cvisi.
DR InterPro; IPR000051; -.
DR InterPro; IPR002052; -.
DR InterPro; IPR002296; -.
DR PRINTS; PR00507; N12N6WTFRASE.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
KW transferase; Methyltransferase.
SQ SEQUENCE 372 AA; 42504 MW; A0F3B94287A2D0D2 CRC64;

Query Match          7.4%; Score 83; DB 14; Length 372;
Best Local Similarity 22.4%; Pred. No. 2.9;
Matches 33; Conservative 29; Mismatches 67; Indels 18; Gaps 5;

QY 32 VFTVATIMVLVQRTDISPNPNVP--LKGGNCSEDLICLKRAPPKSWAVL--QVAK 87
DB 236 VFKVYGMFKTLQ--DYFSRNPHEIPVLUKKDCNKREI-----RFDKRLFDKQIKT 286

QY 88 HLNKTLSWKNKGILHGVRQDGNLVIQFPGLFYICQLQFLVQCNPNSVDLKLLELLINK 147
DB 287 HSGKCILMLRSNGVVMGSEYILRFSESESEFLFDICLVGIFGFDIDKVDLSLDIITSQ 346

QY 148 HIKKQALVTVCESGMOTKHVYQNLQSF 174
DB 347 YLQK-----VCGSGRLTKNIIMNLPF 368

RESULT 15
Q56619          PRELIMINARY;      PRT;      636 AA.
ID Q56619;
AC Q56619;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE O139 ORF1.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A11837;
RX MEDLINE=96417860; PubMed=8820651;
RA Comstock L.E., Michalski J.M., Johnson J.A., Morris J.G. Jr.,
RA Kaper J.B.;
RT "Cloning and sequence of a region encoding a surface polysaccharide of
RT Vibrio cholerae O139 and characterization of the insertion site in the
RT chromosome of Vibrio cholerae O1.";
RL Mol. Microbiol. 19:815-826(1996).
DR EMBL; U47057; AAC46243.1; -.
DR HSSP; P22106; ICT9.
DR InterPro; IPR00583; -.
DR InterPro; IPR001962; -.
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DR Pfam; PF00310; GATase_2; 1.
DR Pfam; PF00733; Asn_synthase; 2. EE80FAE0EA8B1F36 CRC64;
SQ SEQUENCE 636 AA; 71948 MW; EE80FAE0EA8B1F36 CRC64;

Query Match          7.4%; Score 83; DB 2; Length 636;
Best Local Similarity 23.3%; Pred. No. 5.4;
Matches 40; Conservative 22; Mismatches 66; Indels 44; Gaps 5;

QY 58 LKGGNCSEDLICILK-----RAPFKKSWAYLQVAKHLNKTLSWKNKGIL 102
DB 267 LSGGVDSSTVVGIIQLSLSTRPVKFTTIGFDHADFNSEASDVAKHLGTDHV----- 318

QY 103 HGVRYQDGNLVIQFPGLFYICQLQFLVQCNPNSVDLKLLELLINKHIKKQALVTVCESGM 162
DB 319 -----ELIVSAEDALAIINOLPMVYDEPFADASQVPTFLVSKLAKKE--VTVCLSG- 367

QY 163 QTKHVYQNLQFLLDYLVQNTTISVNVDTFOYIDTSTPLENVLSIFLYSNS 214
DB 368 -----DGGDELFCCYNRYHYTAKV----WSYLEKIPPIPKMLSVFLLTIS 409

Search completed: September 5, 2001, 10:29:30
Job time: 405 sec
```

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2001, 10:29:52 ; Search time 19.38 Seconds  
(without alignments)  
380.027 Million cell updates/sec

Title: US-09-628-126-23

Perfect score: 1118  
Sequence: 1 MHPVAGSVASHLGTTSRSYF.....DTSTFPLENLSIFLYNSND 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1118	100.0	234	1 TNF8_HUMAN	P32971 homo sapien
2	814.5	72.9	239	1 TNF8_MOUSE	P32972 mus musculus
3	112	10.0	279	1 FASL_MOUSE	P41047 mus musculus
4	96.5	8.6	234	1 TNFA_HORSE	P29553 equus caball
5	94	8.4	233	1 TNFA_MACMU	P48094 macaca mula
6	94	8.4	235	1 TNFA_PERLE	P36939 peromyscus
7	92	8.2	233	1 TNFA_WACFA	P79337 macaca fasc
8	90.5	8.1	281	1 FASL_HUMAN	P48023 homo sapien
9	90	8.1	233	1 TNFA_PAPHU	O77510 papio hamad
10	90	8.0	233	1 TNFA_PAPSP	P33620 papio sp. (
11	89	8.0	809	1 YATA_SCHPO	Q10155 schizosacch
12	86	7.7	278	1 FASL_RAT	P36940 rattus norv
13	85.5	7.6	309	1 41BL_MOUSE	P41274 mus musculus
14	85	7.6	233	1 TNFA_CANFA	P51742 canis famil
15	85	7.6	235	1 TNFA_MOUSE	P06804 mus musculus
16	85	7.6	1220	1 CSAC_BACTU	P56955 bacillus th
17	84.5	7.6	232	1 TNFA_PIG	P23563 sus scrofa
18	83.5	7.5	234	1 TNFA_SHEEP	P23383 ovis aries
19	83	7.4	1385	1 C5AA_BACUD	O45760 bacillus th
20	81.5	7.3	461	1 IP3K_HUMAN	P23677 homo sapien
21	81	7.2	233	1 TNFA_HUMAN	P31375 homo sapien
22	81	7.2	233	1 TNFA_WARMO	O35734 marmota mon
23	81	7.2	541	1 YHBX_ECOLI	P42640 escherichia
24	81	7.2	1289	1 C5AB_BACUD	O45753 bacillus th
25	80.5	7.2	499	1 PPF5_RAT	P53042 rattus norv
26	80	7.2	229	1 TNFA_CEREL	P51743 cervus elap
27	80	7.2	235	1 TNFA_RAT	P16599 rattus norv
28	79.5	7.1	233	1 TNFA_BOVIN	Q06599 bos taurus
29	79	7.1	800	1 PT11_YEAST	P08468 saccharomyc
30	78.5	7.0	234	1 TNFA_CAVPO	P51435 cavia porce
31	78.5	7.0	426	1 MMML_YEAST	P41800 saccharomyc
32	77.5	6.9	670	1 DD18_HUMAN	Q9nvp1 homo sapien
33	76	6.8	479	1 PAP1_VACCC	P21079 vaccinia vi

34	76	6.8	829	1	TOP1_XENLA	P41512 xenopus lae
35	76	6.8	982	1	MSHM_SARGL	O63852 sarcophyton
36	75.5	6.8	807	1	SUS1_ARATH	P49040 arabidopsis
37	75	6.7	427	1	SYS_BUCAP	P81434 buchnera ap
38	75	6.7	499	1	PPP5_HUMAN	P53041 homo sapien
39	74.5	6.7	745	1	RNR_BUCAI	P57628 buchnera ap
40	74	6.6	851	1	NUD1_YEAST	P32336 saccharomyc
41	74	6.6	2136	1	YCF2_MARPO	P09975 marchantia
42	73.5	6.6	1178	1	PH81_YEAST	P17442 saccharomyc
43	73	6.5	606	1	LEPA_BORBU	O51115 borrelia bu
44	72.5	6.5	1900	1	STT4_YEAST	P37297 saccharomyc
45	72	6.4	221	1	GP53_BPSP1	O48407 bacterioph

#### ALIGNMENTS

RESULT 1  
TNF8\_HUMAN  
ID TNF8\_HUMAN STANDARD; PRT; 234 AA.  
AC P32971;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE CD30 LIGAND (CD30-L) (CD153 ANTIGEN).  
GN TNFSF8 OR CD30LG OR CD30L.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93313964; PubMed=8391931;  
RA Smith C.A., Gruess H.-J., Davis T., Anderson D., Farrah T.,  
RA Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,  
RA Grabstein K.H., Gliniak B., McAllister I.B., Fanslow W., Alderson M.,  
RA Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.;  
RT \*CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose  
RT ligand defines an emerging family of cytokines with homology to  
TNF".  
RL Cell 73:1349-1360(1993).  
CC -!- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF  
CC T CELLS.  
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.  
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD153 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd153.htm".  
CC -----  
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CC -----  
CC EMBL; L09753; AAA74594.1; -  
CC PIR; A40710; A40710.  
CC MIM; 603875; -  
CC InterPro; IPR000478; -  
CC Pfam; PF00229; TNF; 1.  
CC PROSITE; PS00251; TNF\_1; 1.  
CC PROSITE; PS00049; TNF\_2; 1.  
CC Cytokine; Transmembrane; Glycoprotein; Signal-anchor.  
CC DOMAIN 1 37  
CC CYTOPLASMIC (POTENTIAL).  
CC SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
CC TRANSMEM 38 62  
CC DOMAIN 63 234  
CC FT CARBOHYD 81 81 (POTENTIAL).  
CC FT CARBOHYD 109 109 (POTENTIAL).  
CC FT CARBOHYD 153 153 (POTENTIAL).  
CC FT CARBOHYD 189 189 (POTENTIAL).  
CC FT CARBOHYD 201 201 (POTENTIAL).  
CC FT CARBOHYD 234 234 (POTENTIAL).  
CC SEQUENCE 234 AA; 26017 MW; C653615682305B1B CRC64;

Query Match 100.0%; Score 1118; DB 1; Length 234;  
Best Local Similarity 100.0%; Pred. No. 2.3e-97;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSDPNPLKG 60  
DB 20 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSDPNPLKG 79  
QY 61 GNCSEDLICILRAPPKKSWAYLQVAKHLNKTLSNKGILHGVRQDGNLVIOPPGLY 120  
DB 80 GNCSEDLICILRAPPKKSWAYLQVAKHLNKTLSNKGILHGVRQDGNLVIOPPGLY 139  
QY 121 FTICQLQFLVQCPNNSVDLKLLELLINKHKIKQALVTVCSGMQTKHVYQNLQSLFDLYLQ 180  
DB 140 FTICQLQFLVQCPNNSVDLKLLELLINKHKIKQALVTVCSGMQTKHVYQNLQSLFDLYLQ 199  
QY 181 VNTTISVNVDTFQYIDTSTFPLENVLISFLYSNSD 215  
DB 200 VNTTISVNVDTFQYIDTSTFPLENVLISFLYSNSD 234

## RESULT 2

TNF8\_MOUSE  
ID TNF8\_MOUSE STANDARD; PRT; 239 AA.  
AC P32972;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE CD30 LIGAND (CD30-L).  
GN TNFSF8 OR CD30LG OR CD30L.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=T-cell;  
RX MEDLINE=933113964; PubMed=8391931;  
RA Smith C.A., Gruess H.-J., Davis T., Anderson D., Farrah T.,  
RA Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,  
RA Grabstein K.H., Gliniak B., McAllister I.B., Fanslow W., Alderson M.,  
RA Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.;  
RT "CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose  
RT ligand defines an emerging family of cytokines with homology to  
RL Cell 73:1349-1360(1993).  
CC -1- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF  
CC T CELLS.  
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; L09754; AAA74595.1; -;  
DR PIR; B40710; B40710  
DR MGD; MGI:88328; Tnfsf8.  
DR InterPro; IPR000478; -;  
DR Pfam; PF00229; TNF; 1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS00049; TNF\_2; 1.  
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.  
FT DOMAIN 1 43 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 44 67 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
FT DOMAIN 68 239 EXTRACELLULAR (POTENTIAL).  
FT CARBOHYD 75 75 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 114 114 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 158 158 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 194 194 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 206 206 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 239 AA; 26519 MW; 29003157DD425159 CRC64;  
  
Query Match 72.9%; Score 814.5; DB 1; Length 239;  
Best Local Similarity 70.6%; Pred. No. 5.1e-69;  
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

QY 1 MHVPAGSVAS-----HLGTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPD 54  
DB 20 MQVPGSVASVWPRSTRPWRSTRSFYLTATL-VCLVAVAILVLVVKDKSTPNTTE 78  
QY 55 NVPLKGGNCSEDLICILRAPPKKSWAYLQVAKHLNKTLSNKGILHGVRQDGNLV 114  
DB 79 KAPLKGNCSEDLICILRAPPKKSWAYLQVAKHLNKTLSNKGILHGVRQDGNLV 138  
QY 115 QFPGLYFIICQLQFLVQCPNNSVDLKLLELLINKHKIKQALVTVCSGMQTKHVYQNLQSL 174  
DB 139 QFPGLYFIICQLQFLVQCPNNSVDLKLLELLINKHKIKQALVTVCSGMQTKHVYQNLQSL 198  
QY 175 LLDYLVQNTTISVNVDTFQYIDTSTFPLENVLISFLYSNSD 215  
DB 199 LLHYLVQNTTISVNVDTFQYIDTSTFPLENVLISFLYSNSD 239  
  
RESULT 3  
FASL\_MOUSE  
ID FASL\_MOUSE STANDARD; PRT; 279 AA.  
AC P41047; Q61217; Q9R1F2;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE FAS ANTIGEN LIGAND.  
GN TNFSF6 OR APT1LG1 OR FASL OR GLD.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM FASL).  
RX MEDLINE=94185175; PubMed=7511063;  
RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,  
RA Suda T., Nagata S.;  
RT "Generalized lymphoproliferative disease in mice, caused by a point  
RT mutation in the Fas ligand."  
RL Cell 76:969-976(1994).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.  
RC STRAIN=C57BL/6;  
RX MEDLINE=95388076; PubMed=7544870;  
RA Peitsch M.J., Tschoopp J.J.;  
RT "Comparative molecular modelling of the Fas-ligand and other members  
RT of the TNF family".  
RL Mol. Immunol. 32:761-772(1995).  
RN [3],  
RP SEQUENCE FROM N.A. (ISOFORM FASL).  
RX MEDLINE=95196085; PubMed=7889405;  
RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,  
RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;  
RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a  
RT TNF family gene cluster."  
RL Immununity 1:131-136(1994).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM FASL).  
RC STRAIN=BALB/C;  
RA Fenner M.H., Shioda T., Isselbacher K.J.;  
RT "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in  
RT two amino acids."  
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

[5]  
SEQUENCE FROM N.A. (ISOFORM FASLS).  
RC STRAIN=C3H; TISSUE=Spleen;  
RA MEDLINE=20021694; PubMed=10552956;  
RX Aiyolodi E., D'Adamo F., Zollo O., Agostini M., Moraca R.,  
R Cannarile L., Migliorati G., Delfino D.V., Riccardi C.;  
RT "Cloning and expression of a short Fas ligand: A new alternatively  
spliced product of the mouse Fas ligand gene.";  
RL Blood 94:3456-3467(1999).  
[6]  
CHARACTERIZATION OF VARIANT GLD.  
RX MEDLINE=96091792; PubMed=7495745;  
RA Hahne M., Peitsch M.C., Imler M., Schroeter M., Lowin B.,  
R Rousseau M., Bron C., Renno F., French L., Tschoop J.;  
RT "Characterization of the non-functional Fas ligand of gld mice.";  
RL Int. Immunol. 7:1381-1386(1995).  
CC -I- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT  
TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN  
CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.  
CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF  
PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE  
T CELLS, OR BOTH.  
CC -I- SUBUNIT: HOMOTRIMER (PROBABLE).  
CC -I- SUBCELLULAR LOCATION: ISOFORM FASL IS A TYPE II MEMBRANE PROTEIN.  
CC ISOFORM FASLS IS SOLUBLE.  
CC -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS: FASL (SHOWN HERE) AND FASLS; ARE  
PRODUCED BY ALTERNATIVE SPLICING. ISOFORM FASL MEDIATES APOPTOSIS  
WHILE ISOFORM FASLS PREVENTS APOPTOSIS INDUCED BY FAS/FASL  
INTERACTION.  
CC -I- DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERALIZED  
LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DISEASE  
RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION.  
CC -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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-----  
DR EMBL; U06948; AAA17800.1; -;  
DR EMBL; U10984; AAA19778.1; -;  
DR EMBL; S76752; AAB33780.1; -;  
DR EMBL; U58995; AAB02915.1; -;  
DR EMBL; AF119335; AAD52106.1; -;  
DR HSSP; P01375; 2TUN.  
DR MGD; MGI:99255; Fasl.  
DR InterPro; IPR000478; -;  
DR Pfam; PF00229; TNF; 1.  
DR PROSITE; PS00251; TNF.1; 1.  
DR PROSITE; PS50049; TNF.2; 1.  
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis;  
KW Disease mutation; Alternative splicing.  
FT DOMAIN 1 78 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 79 100 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
FT DOMAIN 101 279 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 4 69 PRO-RICH.  
FT DOMAIN 45 51 POLY-PRO.  
FT DISULFID 200 231 BY SIMILARITY.  
FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARSPLIC 1 210 MISSING (IN ISOFORM FASLS).  
FT VARIANT 184 184 T -> A (IN STRAIN BALB/C).  
FT VARIANT 218 218 E -> G (IN STRAIN BALB/C).  
FT VARIANT 273 273 F -> L (IN GLD; ABOLISHES BINDING OF FASL  
TO ITS RECEPTOR).  
SQ SEQUENCE 279 AA; 31442 MW; 37972E2728E0A1CA CRC64;

Query Match 10.0%; Score 112; DB 1; Length 279;  
Best Local Similarity 22.6%; Pred. No. 0.0024;  
Matches 38; Conservative 30; Mismatches 58; Indels 42; Gaps 6;  
QY 33 FTVATIMVLVVQRTDSIPNSPDNVPLKGGNGCEDLLCLIKRAPFKKSWAYLQVAKHLNKT 92  
DB 115 FTQSLKVSFEKQIANPSTPSE-----KKEP--RSVAHLTGPHSRSI 156  
QY 93 KLSWNK---DGILHGVRQDNLVQFPGLYFIICQQLVQ-CPNNSVDLKLLELLINKH 148  
DB 157 PLEWEDTYGTALISGVKYGKGLVINETGLYFVYSKVYFGQSCNNQPLNKHVYMRNSKY 216  
QY 149 -----IKQALVTVCESGM-----QTKHVVYQNLQSOFL 176  
DB 217 PEDLVMEERKRLNYCTTGQIWAHSSYLGAVFNLTSADHLVYNIQSLSL 264  
RESULT 4  
TNFA\_HORSE  
ID TNFA\_HORSE STANDARD; PRT; 234 AA.  
AC P29553;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).  
GN TNF OR TNFA.  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92084125; PubMed=1748301;  
RA Su X., Morris D.D., McGraw R.A.;  
RT "Cloning and characterization of gene TNF alpha encoding equine tumor  
necrosis factor alpha.";  
RL Gene 107:319-321(1991).  
CC -I- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE  
WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF  
CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF  
CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION  
OR BY STIMULATION OF INTERLEUKIN 1 SECRETION. IT CAN STIMULATE  
CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN  
CONDITIONS.  
CC -I- SUBUNIT: HOMOTRIMER.  
CC -I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
EXTRACELLULAR SOLUBLE FORM.  
CC -I- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY  
PROTEOLYTIC PROCESSING.  
CC -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
-----  
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-----  
DR EMBL; M64087; AAA30959.1; -;  
DR PIR; JQ1344; JQ1344.  
DR HSSP; P01375; ITNF.  
DR InterPro; IPR000478; -;  
DR InterPro; IPR002959; -;  
DR Pfam; PF00229; TNF; 1.  
DR PRINTS; PR01234; TNECROSISFCT.  
DR PRINTS; PR01235; TNFALPHA.  
DR PROSITE; PS00251; TNF.1; 1.  
DR PROSITE; PS50049; TNF.2; 1.  
KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.  
FT PROPEP 1 77 BY SIMILARITY.  
FT CHAIN 78 234 TUMOR NECROSIS FACTOR.  
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

FT DISULFID 146 178 BY SIMILARITY.  
SQ SEQUENCE 234 AA; 25469 MW; E79ACE91143DF373 CRC64;

Query Match 8.6%; Score 96.5; DB 1; Length 234;

Best Local Similarity 24.7%; Pred. No. 0.054; 88; Indels 25; Gaps 8;  
Matches 48; Conservative 33; Mismatches

Qy 18 SFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDVPLKGGNCSEDLILCKRAPEK 77

Db 37 SFLLVAGATTFLCLLH-----FGVIGPQREQLPNAFQSI-----NPLAOTLRSSSTPSD 87

Qy 78 KSWAYLQVAKHLNKTLSW---NKDGIL-HGVRYODGNLVIOFPGLYFIICQLQFLVQ-C 132

Db 88 KPAHV-VANPQAEQOLWLSGRANALLANGVKLTQNLVLPVLDGLYLIYSQVLFKGGC 146

Qy 133 PNNSVDL--KLELLINKHKIKQALVCESGMOT-----KHVYONLSQFLLDYLQVN 192

Db 147 PSTHVLTLTISRSLAVSPSKVNLLSAISKSPCHTESPEQAERKPWYPIYLGVGFLQEG 206

Qy 183 TTISVNVDFQYID 196

Db 207 DLSAEINQPNYLD 220

Query Match 8.4%; Score 94; DB 1; Length 233;

Best Local Similarity 25.2%; Pred. No. 0.092;

Matches 51; Conservative 29; Mismatches 80; Indels 42; Gaps 11;

Qy 18 SYFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDV-PLKGGNCSEDLILCKRAPE 76

Db 37 SFLLVAGATTFLCLLH-----FGVIGPQREQLPNAFQSI-----NPLAOTLRSSSTPS 85

Qy 77 KSWAYLQVAKHLNKTLSW-NKDG-----ILHGVRYODGNLVIOFPGLYFIICQLQFLVQ- 131

Db 86 KPAHV-VANPQAEQOLWLSGRANALLANGVKLTQNLVLPVLDGLYLIYSQVLFKGGC 144

Qy 132 CPNNSVDL-----KLELLINKHKIKQALVCE-----SGMOTKHVYONLSQF 174

Db 145 CPNNSVDL-----KLELLINKHKIKQALVCE-----SGMOTKHVYONLSQF 197

Qy 175 LLDYLVQNTTISVNVDFQYID 196

Db 198 GVFLQEGDRLSAEINLPDYLD 219

RESULT 6

TFNA\_PERLE STANDARD; PRT; 235 AA.

AC P36939;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).

TNF OR TNFA.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Macaca.

OX NCBI\_TaxID=9544;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=96003435; PubMed=7561102;

RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;

RT "Comparative sequence analysis of cytokine genes from human and

nonhuman primates.";

RL J. Immunol. 155:3946-3954(1995).

CC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE

CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF

CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF

CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION

CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE

CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN

CC CONDITIONS.

CC -!- SUBUNIT: HOMOTRIMER.

CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN

CC EXTRACELLULAR SOLUBLE FORM.

CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY

CC PROTEOLYTIC PROCESSING.

CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING

CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH

CC AND MALNUTRITION.

CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

DR EMBL; U19850; AAA86712.1;

DR HSSP; P01375; ITNF.



```

FT CARBOHYD      260          N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE     281 AA; 31485 MW;  ABA6EB358246E9BB CRC64;

Query Match           8.1%; Score 90.5; DB 1; Length 281;
Best Local Similarity 26.4%; Pred.No.0.24; Indels 27; Gaps
Matches 34; Conservative 21; Mismatches 47;

QY 75 PFKSKW---AYLQVAKHLNKTLSWNKD-GT--LHGVRQDGNLVIOPPGLYFICQLQF 128
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 138 PEKELRKVAHLTCKSNSRSPLEWDYTGIVLSGVKYKKGLVINETGLIFYYSKVYF 197
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 129 LVQ-CPNNSDVKLKLELINKH-----TKKQALVTVCSGM-----QPKHV 167
    || | | : : : : : | : : : : : | : : : : : | : : : : : | :
DB 198 RQSCNNLPILSHKVMRSNSKYPODLVMMEGKMMSYCITGOMWARSSYLGA VFNLT SADHL 257
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 168 QYNLSQFLL 176
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 258 YVNVSELSL 266
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 9
TNFA_PAPHU
ID TNFA_PAPHU STANDARD; PRT; 233 AA.
AC O77510;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
GN TNF OR TNFA.
OS Papio hamadryas ursinus (Chacma baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=36229;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98147379; PubMed=9488055;
RA Haudek S.B., Redl H., Schlag G., Giroir B.P.;
RT "Complementary DNA (cDNA) sequence of baboon tumor necrosis factor
   alpha."
RL Mol. Immunol. 34:1041-1042(1997).
CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA. IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC CC
CC -1- SUBUNIT: HOMOTRIMER.
CC CC
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC CC
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC CC
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC CC
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
-----
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EMBL: AF019963; AAC31675.1; -.
DR InterPro: IPR000478; -.
DR InterPro: IPR002959; -.
DR Pfam: PR00229; TNF; 1.
DR PRINTS: PR01234; TNECROSISFCT.
DR PRINTS: PR01235; TNFALPHA.

```



DR	HSSP; P01375; TNF.
DR	InterPro; IPR000478; -
DR	InterPro; IPR002959; -
DR	Pfam; PF00229; TNF_1.
DR	PRINTS; PR01234; TNECROSISFCT.
DR	PRINTS; PR01235; TNFALPHA.
DR	PROSITE; PS00251; TNF_1; 1.
DR	PROSITE; PS00049; TNF_2; 1.
KW	Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor;
KW	Myristate.
FT	PROPEP 1 76 BY SIMILARITY.
FT	CHAIN 77 233 TUMOR NECROSIS FACTOR.
FT	TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT	LIPID 19 19 MYRISTATE (BY SIMILARITY).
FT	LIPID 20 20 MYRISTATE (BY SIMILARITY).
FT	DISULFID 145 177 BY SIMILARITY.
SQ	SEQUENCE 233 AA; 25557 MW; 455360B48DC74I73 CRC64;
 Query Match 8.1%; Score 90; DB 1; Length 233; Best Local Similarity 24.8%; Pred. No. 0.22; Matches 50; Conservative 30; Mismatches 80; Indels 42; Gaps 11;	
QY	18 SYFLTTATLALCLVFTVATIMVLVORTDSIPNSPDNV-PLKGGNCSEDLCLKRAPF 76   :        :       :     :     :     :
DB	37 SFLLVAGATTFLCLH-----PGVIPQR-EFFPKDPSLSLAQAVRS-----SRTPS 85
QY	77 KSWAYLOVAKHLNKTLSW-NKGDS---ILHGVRVDGNVLQFPGLYFIICQLQFLVQ- 131   :     :       :     :     :     :
DB	86 DKPAHV-VANPQAEGLQNLNRANALLANGVELRDQNLVVPSEGLYLIYSQVLFRGQG 144
QY	132 CPNNSVDL-----KLELLINKHKKAALVTVC-----SGMOTKHVVQNLSOF 174     :       :     :     :     :     :
DB	145 CPSTHVLTHPTISRIASVYQTKNLL-----SAIKSPQRETPEGEAEPWEPIYL 197 :   :   :   :   :   :   :   :   :   :   :
QY	175 LLDYLQVNTTISVNVDPFQYID 196 :   :   :   :   :   :   :   :   :   :   :
DB	198 GVFOLEKGDRLSAEINLPDYLD 219
 RESULT 11 YATA_SCHPO ID YATA_SCHPO STANDARD; PRT; 809 AA. AC Q10155; DT 01-OCT-1996 (Rel. 34, Created) DT 01-OCT-1996 (Rel. 34, Last sequence update) DT 15-JUL-1998 (Rel. 36, Last annotation update) DE HYPOTHETICAL 90.6 KDA PROTEIN CID4.10 IN CHROMOSOME I. GN SPACID4.10. OC Schizosaccharomyces pombe (Fission yeast). OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; OC Schizosaccharomycetales; Schizosaccharomycetaceae; OC Schizosaccharomycetes. OX NCBI_TaxID=4896; RN [1] RP SEQUENCE FROM N.A. RC STRAIN=972; RA Lye G., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.; RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases. CC -1- SIMILARITY: TO S.POMBE SPBC3D5.03C AND SOME, TO YEAST YKR079C. ----- CC This SWISS-PROT entry is copyright. It is produced through a collaboration CC between the Swiss Institute of Bioinformatics and the EMBL outstation - CC the European Bioinformatics Institute. There are no restrictions on its CC use by non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by and for commercial CC entities requires a license agreement (See http://www.isb-sib.ch/announce/ CC or send an email to license@isb-sib.ch). ----- CC EMBL; Z69239; CAA93219.1; -- DR HSSP; P15039; IPRV. KW Hypothetical protein. SO SEQUENCE 809 AA; 90602 MW; 350FBE7B05FBF880 CRC64;	

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FT CARBOHYD 257      257      N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 278 AA; 31140 MW; 2898E18A862CEAC6 CRC64;

Query Match              7.7%; Score 86; DB 1; Length 278;
Best Local Similarity    23.6%; Pred. No. 0.63;
Matches                  21; Mismatches          49; Indels       24; Gaps           4;

Qy 78 KSWAYLQVAKHLNKTLSWNK----DGILHGVRYQDNLVIOFPGPLFYIFICOLFLVQ-CP 133
   :|:|:|               |::||:|:| ||||: |:|:|:|
Db 141 RSVHALTGNPRSRISPLEWDTYGTALISGVKYKKGLVLNEAGLYFFYSKVYPRGOSCN 200
   :|:|:|               |::||:|:| ||||: |:|:|:|
Qy 134 NNSVDLKLELELNK-----TKKQALVTVCDSGM-----QTKHVYNQLSQ 173
   :|:|:|               |::||:|:| ||||: |:|:|:|
Db 201 SQPLSHKVMRNFKPYPGDVLVMEKKKLNYCTTGQIWAHSSYLGAVFNLTVADHLYVNISQ 260
   :|:|:|               |::||:|:| ||||: |:|:|:|
Qy 174 FLL 176
   |
Db 261 LSL 263

RESULT 13
41BL_MOUSE
ID 41BL_MOUSE STANDARD; PRT; 309 AA.
AC P41274;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 4-LBB LIGAND (4-LBBI).
GN TNFSF9 OR LY63L OR CD137L OR CD157L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=94009225; PubMed=8405064;
RA Goodwin R.G., Din W.S., Davis-Smith T., Anderson D.M., Gimpel S.D.,
RA Sato T.A., Maliszewski C.R., Brannan C.I., Copeland N.G.,
RA Jenkins N.A., Farrar T., Armitage R.J., Fanslow W.C., Smith C.A.;
RT "Molecular cloning of a ligand for the inducible T cell gene 4-1BB: a
RT member of an emerging family of cytokines with homology to tumor
RT necrosis factor.";
RL Eur. J. Immunol. 23:2631-2641(1993).
CC -!- FUNCTION: INDUCES THE PROLIFERATION OF ACTIVATED PERIPHERAL BLOOD
CC T CELLS. MAY HAVE A ROLE IN ACTIVATION-INDUCED CELL DEATH (AICD).
CC MAY PLAY A ROLE IN COGNATE INTERACTIONS BETWEEN T CELLS AND
CC B CELLS/MACROPHAGES.
CC -!- SUBUNIT: HOMODIMER (TYPE II).
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
-----
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-----
EMBL: L15435; AAA39435.1; --
MGD; MG1:1101058; Tnfsf9.
InterPro: IPR000478; -.
Pfam: PF00229; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PSS00049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT DOMAIN 1 82
FT TRANSEM 83 103
FT DOMAIN 104 309
FT CARBOHYD 139 139
FT CARBOHYD 161 161
FT FT
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FT CARBOHYD 293 293 N-LINKED (GLCNAC.....) (POTENTIAL).
SQ SEQUENCE 309 AA: 33853 MW; 2A425829AD6B89C0 CRC64;

Query Match
Best Local Similarity 23.5%; Pred. No. 0.8; Length 309;
Matches 52; Conservative 38; Mismatches 78; Indels 53; Gaps 12;

QY 27 LALCLVFTVATIMLVVQRTDSTP-----NSPDNV-PLKGGNCSEDLCLCIL 71
Db 87 VALVLLLLIAA-CVPIFTREPRPALTTITSPNLGTRENNADQVTPVSHIGCPN---TTQ 142

QY 72 KRAP-FKKSWAYLQVAKHLNKLKLSW-NKDG-----ILHGVRYQDG--NLVIQPPGLYFI 122
Db 143 QGSPVFAKLLARNOAS--LCNTTLNHSQDGAGSSYLSQGLRYEEDKKELVVDSPGLYYV 200

QY 123 IGOLOFLVQCPNN-----SVDLKLELLINKHKKQALVTVCESGMQTKHYVONLSQF 174
Db 201 FLEKLSPTFTTNGHKVQGSVLVLAQKQVDFEDNLALVLEFPSCNENKLVDRWSQL 260

QY 175 LLDYLVQNTTISVNVDTF-----QYIDTSTFPL 202
Db 261 LL--LKAGHRLSVGLRAYLHGAQDAYRDWELSYPTNTSFG 299

RESULT 14
TNFA_CANFA
ID TNFA_CANFA STANDARD; PRT; 233 AA.
AC P51742; Q28339;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
GN TNF OR TNFA.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN SEQUENCE FROM N.A.
RA Fiers W., Beernaert M.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Zucker K., Lu P., Fuller L., Asthana D., Esquenazi V., Miller J.;
RT "Cloning and expression of the cDNA for canine tumor necrosis
RT factor-alpha in E. coli.";
RL Lymphokine Res. 13:191-196(1994).
RN [3]
RP SEQUENCE OF 74-205 FROM N.A.
RC STRAIN-BEAGLE; TISSUE=Blood;
RA Gilmore W.H., Carter S.D., Bennett M., Barnes A., Kelly D.F.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES. IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA, IT IS A POTENT PROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION. IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING (BY SIMILARITY).
CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
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CC -----
DR EMBL; X94932; CAA64403.1; -
DR EMBL; S74068; AAB32391.1; -
DR EMBL; Z70046; CAA93908.1; -
DR HSSP; P01375; ITNF.
DR InterPro; IPR000478; -
DR InterPro; IPR002959; -
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRINTS; PR01235; TNFALPHA.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
FT PROPEP 1 76
FT CHAIN 77 233
FT TRANSMEM 36 56
FT DISULFID 145 177
FT CONFLICT 59 60
FT CONFLICT 66 66
FT CONFLICT 74 74
FT CONFLICT 111 111
FT CONFLICT 116 116
FT CONFLICT 134 135
SQ SEQUENCE 233 AA; 25447 MW; 7B2588FBC8B25340 CRC64;

Query Match 7.6%; Score 85; DB 1; Length 233;
Best Local Similarity 23.8%; Pred. No. 0.64;
Matches 49; Conservative 32; Mismatches 75; Indels 50; Gaps 11;

QY 18 SYFYLTATLALCLVFTVATIMLVVQRTDSTP-----SPDNVPLKGGNCSEDLCLILK 72
Db 37 SFLVAGATTFTCLLH-----FGVIGPQR-EELPNGLQLISPLAQTVKSS-----81

QY 73 RAPEKKSWAYLQVAKHLNKLKLSW---NKDGIL-HGVRYQDGNLVQFPGLYFIICQLQF 128
Db 82 RTPSDKPVAVHV-VANPEAGQLWLSRRANALLANGVELTDQLIVPSDGLIYSQVLF 140

QY 129 LVQ-CPNNSVDL-----KLELLINKHKKQALVTVC-----SGMQTKHYVON 170
Db 141 KGQGCPSHTVLLTHTISRFAVSQYQTKVLL-----SAIKSPCQRETPEGTPEAKPWEP 193

QY 171 LSQFLLDYLVQNTTISVNVDTFQYID 196
Db 194 IYLGGVFQLEKGDRLSABEINLPNYLD 219

RESULT 15
TNFA_MOUSE
ID TNFA_MOUSE STANDARD; PRT; 235 AA.
AC P06804; Q62326;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
GN TNF OR TNFA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RA Shirai T., Shimizu N., Shiojiri S., Horiguchi S., Ito H.;
RT "Cloning and expression in Escherichia coli of the gene for mouse
RT tumor necrosis factor.";
RL DNA 7:193-201(1988).
RN [2]
RP SEQUENCE FROM N.A.
```

RX MEDLINE=85298296; PubMed=3898078;  
 RA Pennica D., Hayflick J.S., Bringham T.S., Palladino M.A.,  
 RA Goeddel D.V.;  
 RT "Cloning and expression in *Escherichia coli* of the cDNA for murine  
 RT tumor necrosis factor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:6060-6064(1985).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86149365; PubMed=2419912;  
 RA Caput D., Beutler B., Hartog K., Thayer R., Brown-Shimer S.,  
 RA Cerami A.;  
 RT "Identification of a common nucleotide sequence in the  
 RT 3'-untranslated region of mRNA molecules specifying inflammatory  
 RT mediators.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:1670-1674(1986).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85242112; PubMed=2989794;  
 RA Fransen L., Mueller R., Marmenout A., Tavernier J., van der Heyden J.,  
 RA Kawashima E., Chollet A., Tizard R., van Heuverswyn H., van Vliet A.,  
 RA Ruysschaert M.-R., Fiers W.;  
 RT "Molecular cloning of mouse tumour necrosis factor cDNA and its  
 RT eukaryotic expression.";  
 RL Nucleic Acids Res. 13:4417-4429(1985).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87298639; PubMed=3040015;  
 RA Shakhov A.N., Nedospasov S.A.;  
 RT "Molecular cloning of genes coding for tumor necrosis factor.  
 RT Complete nucleotide sequence of the genome copy of TNF-alpha in  
 RT mice.";  
 RL Bioorg. Khim. 13:701-705(1987).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88067722; PubMed=3684584;  
 RA Senon D., Kawashima E., Jongeneel C.V., Shakhov A.N., Nedospasov S.A.;  
 RT "Nucleotide sequence of the murine TNF locus, including the TNF-alpha  
 RT (tumor necrosis factor) and TNF-beta (lymphotoxin) genes.";  
 RL Nucleic Acids Res. 15:9083-9084(1987).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CTS, AND NOD;  
 RX MEDLINE=96013654; PubMed=7560085;  
 RA Ikegami H., Makino S., Yamato E., Kawaguchi Y., Ueda H., Sakamoto T.,  
 RA Takekawa K., Ogihara T.;  
 RT "Identification of a new susceptibility locus for insulin-dependent  
 RT diabetes mellitus by ancestral haplotype congenic mapping.";  
 RL J. Clin. Invest. 96:1936-1942(1995).  
 RN [8]  
 RP SEQUENCE OF 80-99.  
 RX MEDLINE=91097531; PubMed=2268312;  
 RA Sherry B., Juc D.-M., Zentella A., Cerami A.;  
 RT "Characterization of high molecular weight glycosylated forms of  
 RT murine tumor necrosis factor.";  
 RL Biochem. Biophys. Res. Commun. 173:1072-1078(1990).  
 RN [9]  
 RP SEQUENCE OF 70-87.  
 RX MEDLINE=89380231; PubMed=2777790;  
 RA Cseh K., Beutler B.;  
 RT "Alternative cleavage of the cachectin/tumor necrosis factor  
 RT propeptide results in a larger, inactive form of secreted protein.";  
 RL J. Biol. Chem. 264:16256-16260(1989).  
 RN [10]  
 RP IDENTIFICATION OF MEMBRANE-BOUND FORM.  
 RX MEDLINE=88165056; PubMed=3349526;  
 RA Kriegler M., Perez X., Defay K., Albert I., Lu S.D.;  
 RT "A novel form of TNF/cachectin is a cell surface cytotoxic  
 RT transmembrane protein: ramifications for the complex physiology of  
 RT TNF.";  
 RL Cell 53:45-53(1988).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS) OF 80-235.  
 RX MEDLINE=99190964; PubMed=10089307;

RA Basyens K.J., De Bondt H.L., Raeymaekers A., Fiers W., De Ranter C.J.;  
 RT "The structure of mouse tumour-necrosis factor at 1.4 A resolution:  
 RT towards modulation of its selectivity and trimerization.";  
 RL Acta Crystallogr. D 55:772-778(1999).  
 CC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE  
 CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF  
 CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF  
 CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION  
 CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE  
 CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN  
 CC CONDITIONS.  
 CC -!- SUBUNIT: HOMOTRIMER.  
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
 CC EXTRACELLULAR SOLUBLE FORM.  
 CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY  
 CC PROTEOLYTIC PROCESSING.  
 CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
 CC AND MALNUTRITION.  
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC -----  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 DR EMBL; U06950; AAA18594.1; -;  
 DR EMBL; M13049; AAA40457.1; -;  
 DR EMBL; M11731; AAA40458.1; -;  
 DR EMBL; Y00467; CAA68530.1; -;  
 DR EMBL; X02611; CAA28457.1; -;  
 DR EMBL; M20155; AAA40462.1; ALT\_SEQ.  
 DR EMBL; M38296; AAA40459.1; -;  
 DR EMBL; D84196; BAA19512.1; -;  
 DR EMBL; D84194; BAA19512.1; JOINED.  
 DR EMBL; D84195; BAA19512.1; JOINED.  
 DR EMBL; D84199; BAA19513.1; -;  
 DR EMBL; D84197; BAA19513.1; JOINED.  
 DR EMBL; D84198; BAA19513.1; JOINED.  
 DR PIR; A23127; QWMSN.  
 DR PIR; A22908; A22908.  
 DR PIR; A25164; A25164.  
 DR PIR; A27303; A27303.  
 DR PIR; A34251; A34251.  
 DR PIR; S03791; S03791.  
 DR PDB; 2TNF; 12-OCT-99.  
 DR MGD; MGI:104798; Tnf.  
 DR InterPro; IPR000478; Tnf.  
 DR InterPro; IPR002959; -;  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR PRINTS; PR01235; TNFALPHA.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor;  
 KW 3D-structure.  
 FT PROPEP 1 79  
 FT CHAIN 80 235  
 FT TRANSMEM 36 56  
 FT DISULFID 148 179  
 FT CARBOHYD 86 86  
 FT CONFLICT 231 231  
 SQ SEQUENCE 235 AA; 25895 MW; 16DD2A9676D68C5D CRC64;

Query Match 7.6%; Score 85; DB 1; Length 235;  
 Best Local Similarity 23.0%; Pred. No. 0.64; Indels 36; Gaps 8;  
 Matches 46; Conservative 31; Mismatches 87;  
 QY 18 SYFYLTATLALCLVFTVATIMVLVQRTDSIPNSPQNVPLKGGNCSEDLICLKRAPFK 77

```

Db 37 SFLVAGATTLECLL-----NFGVIGPQDEKFPN---GLPLISSMAQTTLTRSSSQSSD 89
QY 78 KSMAYLQVAKHLNKTLSWNKDG-----ILHGVRYQDGNLVIOFPGLYFIICQLQFLVQ-C 132
Db 90 KPVARH-VANHQVEQELEWLSORANALLANGMDLKDNLVVPADGLYLVYSQVLFKGGC 148
QY 133 PNN-----SVDLKLELLINKHIKKOALVTVC-----ESGMQTKHVYQNLQFL 176
Db 149 PDYVLLTHTVSRFAISYOEKVNLL-----SAVKSPCKDTPEGAELKPWYEPYILGGV 201
QY 177 DYLOVNTTISVNVDTFOYID 196
Db 202 FQLEKGDQLSAEVNLPKYID 221

```

Search completed: September 5, 2001, 10:29:53  
Job time: 398 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2001, 10:23:52 ; Search time 31.97 Seconds  
(without alignments)  
512.278 Million cell updates/sec

Title: US-09-628-126-23  
Perfect score: 1118  
Sequence: 1 MHPAGSVASHLGTTSRSYF.....DTSTFPLENVLISFLYSNSD 215

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1118	100.0	234	2	CD30 ligand - huma
2	814.5	72.9	239	2	CD30 ligand - mous
3	112	10.0	279	2	Fas ligand - mouse
4	96.5	8.6	234	1	tumor necrosis fac
5	94	8.4	235	2	tumor necrosis fac
6	93.5	8.4	547	2	rifampicin resista
7	90.5	8.1	281	2	Fas ligand - human
8	90	8.1	233	1	tumor necrosis fac
9	89	8.0	809	2	hypothetical prote
10	87.5	7.8	813	2	hypothetical prote
11	86	7.7	278	2	fal ligand - rat
12	85.5	7.6	309	2	4-1BB ligand - mou
13	85	7.6	235	1	tumor necrosis fac
14	84.5	7.6	232	1	tumor necrosis fac
15	83.5	7.5	234	1	tumor necrosis fac
16	83	7.4	636	2	hypothetical prote
17	83	7.4	1385	2	paraspinal crystal
18	82	7.3	513	2	hypothetical prote
19	82	7.3	1339	2	hypothetical prote
20	81.5	7.3	461	2	ID-myo-inositol-tr
21	81	7.2	233	1	tumor necrosis fac
22	81	7.2	547	2	hypothetical 61.6
23	81	7.2	1289	2	paraspinal crystal
24	80.5	7.2	430	2	ORF MSV157 hypothe
25	80.5	7.2	434	1	hypothetical prote
26	80.5	7.2	499	2	phosphoprotein pho
27	80	7.2	235	2	tumor necrosis fac
28	79.5	7.1	233	1	tumor necrosis fac
29	79	7.1	800	2	PET111 protein - y

30 78.5 7.0 426 2 S64748  
31 78.5 7.0 1130 2 T29089  
32 78.5 7.0 1830 2 E82909  
33 77.5 6.9 492 2 S42735  
34 77.5 6.9 610 2 S71758  
35 77.5 6.9 623 2 B96681  
36 77 6.9 329 2 T28412  
37 77 6.9 456 2 B96688  
38 76.5 6.8 478 2 T27714  
39 76.5 6.8 619 2 S54636  
40 76.5 6.8 3512 2 T17121  
41 76 6.8 467 2 D86485  
42 76 6.8 479 2 E42508  
43 76 6.8 607 2 E70165  
44 76 6.8 829 2 S72366  
45 75.5 6.8 284 2 F81431

## ALIGNMENTS

RESULT 1  
A40710  
CD30 ligand - human  
C:Species: Homo sapiens (man)  
C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 21-Jul-2000  
C:Accession: A40710  
R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrar, T.; Baker, E.; Sutherland, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, Cell 73, 1349-1360, 1993  
A:Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de  
A:Reference number: A40710; MUID:93313964  
A:Accession: A40710  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-234 <SMI>  
A:Cross-references: GB:L09753; NID:g349277; PIDN:AAA74594.1; PID:g349278  
C:Keywords: cytokine receptor; membrane protein; surface antigen

Query Match 100.0%; Score 1118; DB 2: Length 234;  
Best Local Similarity 100.0%; Pred. No. 2.4e-98;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHPAGSVASHLGTTSRSYFYITTTATLALCLVFTVATIMLVVQRTDSIPNSPDNVLK 60  
Db 20 MHPAGSVASHLGTTSRSYFYITTTATLALCLVFTVATIMLVVQRTDSIPNSPDNVLK 79  
Qy 61 GNCSEDLCLILKRAPFKKSWAYLQVAKHLNKTLSNKGILHGVRYQDGNLVIQPGILY 120  
Db 80 GNCSEDLCLILKRAPFKKSWAYLQVAKHLNKTLSNKGILHGVRYQDGNLVIQPGILY 139  
Qy 121 FICLOQLVQCPNNSVDLKLLELNKHKHKKOALVTVCESGMQTHVYONLSQFLDLVLO 180  
Db 140 FICLOQLVQCPNNSVDLKLLELNKHKHKKOALVTVCESGMQTHVYONLSQFLDLVLO 199  
Qy 181 VNTISVNDVDFQYIDTSTFPLENVLSIFLYSNSD 215  
Db 200 VNTISVNDVDFQYIDTSTFPLENVLSIFLYSNSD 234

## RESULT 2

B40710  
CD30 ligand - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 05-Nov-1999  
C:Accession: B40710  
R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrar, T.; Baker, E.; Sutherland, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, Cell 73, 1349-1360, 1993  
A:Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de  
A:Reference number: A40710; MUID:93313964  
A:Accession: B40710

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-239 <SMI>  
A:Cross-references: GB:L09754; NID:g349288; PIDN:AAA74595.1; PID:g349289  
C:Keywords: cytokine receptor; membrane protein; surface antigen

Query Match 72.9%; Score 814.5; DB 2; Length 239;  
Best Local Similarity 70.6%; Pred. No. 1.2e-69;  
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

Qy 1 MHVPAGSVAS-----HLGTTSSRYFLTTATLALCLVFTVATIMVLVQRTDSIPNSPD 54

Db 20 MQVQPSVASPWRSTRPWRSTRSYFYLTAL-VCLVAVAILVLVQKDDSTPNTTE 78

Qy 55 NVPLKGGNCSEDLILCRAPFKSWAYLOVAKHLNKTLSNKGDLILHGVRQDGNLVI 114

Db 79 KAPLKGNCSEDLFTLKTSPKSWAYLOVSKHLNNTKLSWNEDTIGLIYQDGNLIV 138

Qy 115 QPGLYFIICQLQFLVQCPNNSVDLKLLELNKHKQALVTVCSGMOTKHVYQNLQSF 174

Db 139 QPGLYFIICQLQFLVQCSNHSVDLTQLLINSKIKKQTLVTVCSGVSKNIYQNLQSF 198

Qy 175 LLDYLVQNTTISVNVDTFYIDTSTFPLENVLISFIYNSND 215

Db 199 LLHYLVQNTTISVRVDNFQYVDTNTPFLDNVLSVFLYSSSD 239

RESULT 3

A53062

Fas ligand - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999

C:Accession: A53062

R:Takanashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nag

Cell 76, 969-976, 1994

A:Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in

A:Reference number: A53062; MUID:94185175

A:Accession: A53062

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-279 <TAK>

A:Cross-references: GB:U06948; NID:g473564; PIDN:AAA17800.1; PID:g473565

Query Match

Best Local Similarity 10.0%; Score 112; DB 2; Length 279;

Matches 38; Conservative 30; Mismatches 58; Indels 42; Gaps 6;

Qy 33 FTVATIMVLVQRTDSIPNSPDNVLKGGNCSEDLILCRAPFKSWAYLOVAKHLNKT 92

Db 115 FTNQLKVSSEFKQIANSTPSE-----KKEP--RSVAHLTGPHRSRI 156

Qy 93 KLSNWK---DGLHGVRQDGNLVIQFPGLYFIICQLQFLVQ-CPNNSVDLKLLELNKH 148

Db 157 PLENDYGTALISGVKKYKGLVNETGLVYFVSKVYFRGQSCNQPLNKHVYMRNSKY 216

Qy 149 -----IKKQALVTVCSGM-----OTKHVYQNLQSFLL 176

Db 217 PEDLVLMEEKRLNCTTGQIWAHSSYLGAVFNLTSDHLVYNISQLS 264

RESULT 4

JQ1344

tumor necrosis factor alpha precursor - horse

N:Alternate names: cachectin; TNF alpha

C:Species: Equus caballus (domestic horse)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000

C:Accession: JQ1344

R:Su, X.; Morris, D.D.; McGraw, R.A.

Gene 107, 319-321, 1991

A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis

A:Reference number: JQ1344; MUID:92084125

A:Accession: JQ1344

A:Molecule type: DNA

A:Residues: 1-234 <SUX>

A:Cross-references: GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245

C:Comment: This protein is an important proximal mediator of endotoxemia.

C:Genetics:

A:Gene: TNF-alpha

A:Introns: 62/3; 79/1; 95/1

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m

F:19,20/Binding site: myristate (lys) (covalent) #status predicted

F:82/Binding site: myristate (lys) (covalent) #status predicted

F:146-178/Disulfide bonds: #status predicted

Query Match 8.6%; Score 96.5; DB 1; Length 234;

Best Local Similarity 24.7%; Pred. No. 0.1;

Matches 48; Conservative 33; Mismatches 88; Indels 25; Gaps 8;

Qy 18 SYFYLTTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLKGGNCSEDLILCRAPFK 77

Db 37 SFLLVAGATTFLCLH----FGVIGPOREBPQFQSI-----NPLAQTLRSSRTPSD 87

Qy 78 KSWAYLOVAKHLNKTLSW---NKDGL-HGVRYQDGNLVIQFPGLYFIICQLQFLVQ-C 132

Db 88 KPAHV-VANPQAEQQLWLSGRANALLANGVKLTNDQLVPLDGLVLYSQVLFKGGC 146

Qy 133 PNNSVDL--KLELLINKHKQALVTVCSGMQT-----KHVYQNLQSFLLDYLVQVN 182

Db 147 PSTHVLTTHTISRLAVSPYKVNLLSAIKSPCHTESPEQAEAKPWEPYILGVGVQLEKG 206

Qy 183 TTISVNVDTFYID 196

Db 207 DQLSAEINQPNYLD 220

RESULT 5

I54490

tumor necrosis factor alpha precursor - white-footed mouse

C:Species: Peromyscus leucopus (white-footed mouse)

C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 04-Feb-2000

C:Accession: I54490

R:Crew, M.D.; Filipowsky, M.E.

Immunogenetics 35, 351-353, 1992

A:Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus l

A:Reference number: I54490; MUID:92218012

A:Accession: I54490

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-235 <RES>

A:Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507

C:Genetics:

A:Gene: TNF

A:Introns: 62/3; 81/1; 97/1

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation

F:19,20/Binding site: myristate (lys) (covalent) #status predicted

F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 8.4%; Score 94; DB 2; Length 235;

Best Local Similarity 24.0%; Pred. No. 0.18;

Matches 48; Conservative 31; Mismatches 85; Indels 36; Gaps 8;

Qy 18 SYFYLTTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLKGGNCSEDLILCRAPFK 77

Db 37 SFLLVAGATTFLCLH----NFGVIGPOREBPQFQSI-----NPLIIGSMAQTTLTRSSSSQSSD 89

Qy 78 KSWAYLOVAKHLNKTLSWKNKG-----ILHGVRQDGNLVIQFPGLYFIICQLQFLVQ-C 132

Db 90 KPAHV-VANHQVDEQLEWLSRGNALLANGMDLKNQLVTPADGLVLYSQVLFKGGC 148

[illegible]



```

Db      461 LALCSADSVAFPVLTHTSTRNGLPDHTDPE-----DNEIVCFLK-----VQIA 502
Qy      87 KHLNKTLSNWNKGOILHGVRQDGNLVQIPGLYFIQCQLQFLVQCPNNSVDLKLLELIN 146
Db      503 EAIN-----LQDNLMMAQLQETMRCVCF-----DNRTCKLLASIA 539
Qy      147 KHIKKQ----ALVTVCESGMOT--KHVYQNLQSFLLDYLQVN--TTISVN----- 188
Db      540 EDYKRAPYIAYLTRCRQGLTQTQAHLERLQVRLDKEVANYRFTVCVRLLESKEKK 599
Qy      189 ----VDTFQVI---DTSTFFPLENVLSIFLY 211
Db      600 IREFIQDFOKLTAADDKTAQVEDFLQ-FLY 628

RESULT 11
A49266
C: Species: Rattus norvegicus (Norway rat)
C: Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1995
C: Accession: A49266
R: Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
Cell 75, 1169-1178, 1993
A: Title: Molecular cloning and expression of the Fas ligand, a novel member
A: Reference number: A49266; MUID:94084792
A: Accession: A49266
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-278 <SD>
A: Cross-references: GB:U03470; NID:g440178; PIDN:AAC52129.1; PID:g440179
C: Keywords: glycoprotein; transmembrane protein

```

Query Match	7.74;	Score 86;	DB 2;	Length 278;
Best Local Similarity	23.6%;	Pred. No. 1.2;		
Matches	29;	Conservative 21;	Mismatches 49;	Indels 24;
Gaps				
QY	78	KSWAYLQVAKHLNKTLSWNK---	DGILHGVRVQDGNLVIOFPGLFYFICQLQFLVQ--CP	133
		: : :	: : :	: : :
Db	141	RSVAHLTGNPRSRISPLEWDTYGTALISGVYKRYKGGVLVINEAGLYFYVSKVYFRGQSCN		200
		: : :	: : :	: : :
QY	134	NNSVDLKLLELNKH-----	IKKQALVTVCSGM-----	QTKHVVYONLSQ
		: : :	: : :	: : :
Db	201	SQPLSHRVYMRNFYPGDVLVMEKKLNYCTTGQIWAHSSYLGAVFNLTVADHLVYNISQ		260
QY	174	FLL	176	
bb	261	LSL	263	

Db 261 LSL 263

RESULT 12  
I53384  
4-1BB ligand - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
C:Accession: I53384  
R:Goodwin, R.G.; Din, W.S.; Davis-Smith, T.; Anderson, D.M.; Gimpel, S.D.; Sato, T.A.  
Eur. J. Immunol. 23, 2631-2641, 1993  
A:Title: Molecular cloning of a ligand for the inducible T cell gene 4-1BB: a member  
A:Reference number: I53384; MUID:94009225  
A:Accession: I53384  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-309 <RES>  
A:Cross-references: GB:I51435; NID:q435596; PIDN:AAA39435.1; PID:q435997

Query Match 7.6%; Score 85.5; DB 2; Length 309;  
Best Local Similarity 23.5%; Pred. No. 1.6;  
Matches 52; Conservative 38; Mismatches 78; Indels 53; Gaps 12;  
QY 27 LALCLVFTVATIMVLVQRTDISP-----NSPDNV-PLKGGNCSEDLICIL 71

A:Title: Identification of a common nucleotide sequence in the 3'-untranslated region  
A:Reference number: I59058; MUID:86149365  
A:Accession: I59058  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: rRNA  
A:Residues: 1-230, 'R', 232-235 <RES>  
A:Cross-references: GB:M13049; NID:g202082; PIDN:AAAA0457.1; PID:g202083  
R:Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.  
Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990  
A:Title: Characterization of high molecular weight glycosylated forms of murine tumor  
A:Reference number: A36696; MUID:91097531  
A:Accession: A36696  
A:Molecule type: protein  
A:Residues: 80-85, 'X', 87-99 <SHE>  
C:Genetics:  
A:Introns: 62/3; 81/1; 97/1

A; INTRONS: 62/3; 81/1; 9/1 .  
A: Note: the first intron occurs in the 5'-untranslated region

C;Superfamily: tumor necrosis factor  
C;Role: the first intron occurs in the 5' untranslated region  
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; macrophage; m  
F;80-235/Product: tumor necrosis factor #status experimental <MAT>  
F;20/Binding site: myristate (lys) (covalent) #status predicted  
F;84/Binding site: carboxylate (Ser) (covalent) #status predicted  
F;86/Binding site: carboxylate (Asn) (covalent) #status predicted  
F;148-179/Disulfide bonds: #status predicted

Query Match	7.6%	Score 85;	DB 1;	Length 235;
Best Local Similarity	23.0%;	Pred. No. 1.3;		
Matches	45;	Conservative	31;	Mismatches 87;
				Indels 36;
				Gaps 8;

```

RESULT 14
S12606
tumor necrosis factor alpha precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: S12606; S17290; S18965; I46659
R:Brews, R.T.: Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.
Nucleic Acids Res. 18, 5564, 1990
A:Title: Gene sequence of porcine tumor necrosis factor alpha.
A:Reference number: S12606; MUID:91016861

```

A;Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative analysis  
A;Reference number: S17289; MUID:91340150  
A;Accession: S17290  
A;Molecule type: DNA  
A;Residues: 1-232 <KUH>  
A;Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38639, 1; PID:g2134  
A;Note: the authors translated the codon GAG for residue 202 as Gly  
R;Choi, C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, M.P.  
submitted to the EMBL data Library, January 1991  
A;Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis

A:Reference number: S18965

A:Accession: S18965

A:Molecule type: mRNA

A:Residues: 1-232 <CHO>

A:Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID:g2138

R:Pauli, U.; Beutler, B.; Peterhans, E.

Gene 81, 185-191, 1989

A:Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reaction

A:Reference number: I46659; MUID:90034181

A:Accession: I46659

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 44-232 <PAU>

A:Cross-references: GB:M29079; NID:g164694; PIDN:AAA31128.1; PID:g164695

C:Genetics:

A:Introns: 62/3; 78/1; 93/1

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; myrl

F:1-77/Domain: propeptide #status predicted <PRO>

F:78-232/Product: tumor necrosis factor alpha #status predicted <MAT>

F:19,20/Binding site: myristate (Lys) (covalent) #status predicted

F:81/Binding site: carboxylate (Ser) (covalent) #status predicted

F:144-176/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 7.6%; Score 84.5; DB 1; Length 232;

Matches 45; Conservative 35; Mismatches 79; Indels 43; Gaps 9;

QY 18 SYFYLTATLALCLVFTVATIMLVVQRTDSIPNSPDV-PLKGGNCSEDLCLIKRAPF 76

DB 37 SFLVAGATTFLCLH- - - - -FGVIGPQKEEFPAGPLSINPLAQGLRSS- - - - -QTS 84

QY 77 KKSWAYLOVAKHLNKTLSWKNKG- - - - -ILHGVRVODGNLVIOFPGLYFIICQLQFLVQ- 131

DB 85 DRPVAHV-VANVKAEGQLQWQSYANALLANGVKLDNQLVPTDGLYLIYSQVLFRRGQ 143

QY 132 CPNNSVDL- - - - -KLELLINKHIKKQALVTICE- - - - -SGMOTKHVYQNLISQF 174

DB 144 CPSTNVLFTHTISRTAVSVQTKVNL- - - - -SAIKSPQRETPEGAEPWYPIYLG 196

QY 175 LLDYLQVNTTISVNVDTFOYID 196

DB 197 GVFOLEKGDRLSAEINLPDYLD 218

RESULT 15

JH0529

tumor necrosis factor alpha precursor - sheep

N:Alternate names: cachectin; TNF alpha

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000

C:Accession: JH0529; S48118; S13114; S20661

R:Green, I.R.; Sargan, D.R.

Gene 109, 203-210, 1991

A:Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems with

A:Reference number: JH0529; MUID:92112044

A:Accession: JH0529

A:Molecule type: mRNA

A:Residues: 1-234 <GRE>

A:Cross-references: EMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406

A:Experimental source: alveolar macrophage

R:Nash, A.D.; Barcham, G.J.; Brandon, M.R.; Andrews, A.E.

Immunol. Cell Biol. 69, 273-283, 1991

A:Title: Molecular cloning, expression and characterization of ovine TNF-alpha.

A:Reference number: S48118; MUID:92155784

A:Accession: S48118

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-234 <NAS>

A:Cross-references: EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PID:g297807

R:Young, A.J.; Hay, J.B.; Chan, J.Y.C.

Nucleic Acids Res. 18, 6723, 1990

A:Title: Primary structure of ovine tumor necrosis factor alpha cDNA.

A:Reference number: S13114; MUID:91067496

A:Accession: S13114

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-62,64-234 <YOU>

A:Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404

A:Note: comparison with the introns of homologous sequences suggest that this is prob

C:Superfamily: tumor necrosis factor

C:Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein; lym

F:1-77/Domain: propeptide #status predicted <PRO>

F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>

F:20/Binding site: myristate (Lys) (covalent) #status predicted

F:82/Binding site: carboxylate (Ser) (covalent) #status predicted

F:96/Binding site: carboxylate (Asn) (covalent) #status predicted

F:146-178/Disulfide bonds: #status predicted

Query Match 7.5%; Score 83.5; DB 1; Length 234;

Best Local Similarity 23.3%; Pred. No. 1.7;

Matches 47; Conservative 29; Mismatches 85; Indels 41; Gaps 9;

QY 18 SYFYLTATLALCLVFTVATIMLVVQRTDSIPNSPD-NVPLKGGNCSEDLCLIKRAPF 76

DB 37 SFLVAGATTFLCLH- - - - -FGVIGPQREEQSPAGPSFNRPL- - - - -VQTLRSSQASN 86

QY 77 KKSWAYLOVAKHLNKTLSWKNKG- - - - -ILHGVRVODGNLVIOFPGLYFIICQLQFLVQ- 131

DB 87 NKPAHV-VANISAPQLRWGDSYANALMANGVELKDNLVPTDGLYLIYSQVLFRRHG 145

QY 132 CPNN- - - - -SVDLKLLELLINKHIKKQALVTICE- - - - -SGMOTKHVYQNLISQF 174

DB 146 CPSTPLFTHTISRTAVSVQTKVNL- - - - -SAIKSPCHRETLLEGAEAKPWYPIYQG 198

QY 175 LLDYLQVNTTISVNVDTFOYID 196

DB 199 GVFOLEKGDRLSAEINLPDYLD 220

Search completed: September 5, 2001, 10:23:53

Job time: 123 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2001, 10:23:11 ; Search time 25.09 seconds  
(without alignments)  
176.442 Million cell updates/sec

Title: US-09-628-126-23  
Perfect score: 1118  
Sequence: 1 MHPAGSVASHLGTTSRSYF.....DTSTFPLENVLISFLYNSD 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/2/iaa/5A-COMB.pep:\*

2: /cgn2\_6/ptodata/2/iaa/5B-COMB.pep:\*

3: /cgn2\_6/ptodata/2/iaa/6A-COMB.pep:\*

4: /cgn2\_6/ptodata/2/iaa/6B-COMB.pep:\*

5: /cgn2\_6/ptodata/2/iaa/PCTUS-COMB.pep:\*

6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1118	100.0	215	1 US-08-225-989-23	Sequence 23, Appl
2	1118	100.0	215	1 US-08-570-923-23	Sequence 23, Appl
3	1118	100.0	215	1 US-08-580-014-23	Sequence 23, Appl
4	1118	100.0	215	4 US-09-079-785-23	Sequence 23, Appl
5	1118	100.0	234	1 US-08-225-989-8	Sequence 8, Appl
6	1118	100.0	234	1 US-08-570-923-8	Sequence 8, Appl
7	1118	100.0	234	1 US-08-580-014-8	Sequence 8, Appl
8	1118	100.0	234	4 US-09-079-785-8	Sequence 8, Appl
9	814.5	72.9	220	1 US-08-225-989-19	Sequence 19, Appl
10	814.5	72.9	220	1 US-08-570-923-19	Sequence 19, Appl
11	814.5	72.9	220	1 US-08-580-014-19	Sequence 19, Appl
12	814.5	72.9	220	4 US-09-079-785-19	Sequence 19, Appl
13	814.5	72.9	239	1 US-08-225-989-6	Sequence 6, Appl
14	814.5	72.9	239	1 US-08-570-923-6	Sequence 6, Appl
15	814.5	72.9	239	1 US-08-580-014-6	Sequence 6, Appl
16	814.5	72.9	239	4 US-09-079-785-6	Sequence 6, Appl
17	775	69.3	148	3 US-08-584-031-12	Sequence 12, Appl
18	592	53.0	125	1 US-08-225-989-20	Sequence 20, Appl
19	592	53.0	125	1 US-08-570-923-20	Sequence 20, Appl
20	592	53.0	125	1 US-08-580-014-20	Sequence 20, Appl
21	592	53.0	125	4 US-09-079-785-20	Sequence 20, Appl
22	447.5	40.0	130	1 US-08-225-989-21	Sequence 21, Appl
23	447.5	40.0	130	1 US-08-570-923-21	Sequence 21, Appl
24	447.5	40.0	130	1 US-08-580-014-21	Sequence 21, Appl
25	447.5	40.0	130	4 US-09-079-785-21	Sequence 21, Appl
26	274	24.5	52	4 US-09-369-494-17	Sequence 17, Appl
27	102	9.1	279	5 PCT-US95-00362-5	Sequence 5, Appl

28 92 8.2 378 3 US-08-630-172-21 Sequence 21, Appl  
29 91.5 8.2 376 3 US-08-731-512-8 Sequence 8, Appl  
30 90.5 8.1 145 3 US-08-630-172-5 Sequence 5, Appl  
31 90.5 8.1 179 3 US-08-649-100-9 Sequence 9, Appl  
32 90.5 8.1 281 2 US-08-810-453-2 Sequence 2, Appl  
33 90.5 8.1 281 3 US-08-815-190A-2 Sequence 2, Appl  
34 90.5 8.1 281 4 US-08-290-640-25 Sequence 25, Appl  
35 90.5 8.1 281 4 US-09-479-524-3 Sequence 3, Appl  
36 90.5 8.1 281 5 PCT-US95-00362-2 Sequence 2, Appl  
37 90.5 8.1 287 3 US-08-815-190A-16 Sequence 16, Appl  
38 90 8.1 149 3 US-08-584-031-17 Sequence 17, Appl  
39 86 7.7 158 1 US-07-994-469A-99 Sequence 99, Appl  
40 85.5 7.6 309 1 US-08-236-918A-2 Sequence 2, Appl  
41 85 7.6 161 1 US-07-994-469A-61 Sequence 61, Appl  
42 85 7.6 162 1 US-07-994-469A-60 Sequence 60, Appl  
43 85 7.6 163 1 US-07-994-469A-64 Sequence 64, Appl  
44 85 7.6 235 4 US-08-883-086-7 Sequence 7, Appl  
45 85 7.6 1220 1 US-08-158-232-43 Sequence 43, Appl

#### ALIGNMENTS

RESULT 1  
US-08-225-989-23  
; Sequence 23, Application US/08225989  
; Patent No. 5480981  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644

```

; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 889,717
;   FILING DATE: 26-MAY-1992
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Seese, Kathryn A.
;     REGISTRATION NUMBER: 32,172
;     REFERENCE/DOCKET NUMBER: 2804-E
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (206)587-0430
;     TELEFAX: (206)233-0644
;     TELEX: 756822
;   INFORMATION FOR SEQ ID NO: 23:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 215 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
;   US-08-570-923-23

Query Match          100.0%; Score 1118; DB 1; Length 215;
Best Local Similarity 100.0%; Pred. No. 5.9e-114; Mismatches 0; Indels 0; Gaps 0;
Matches 215; Conservative 0;

Qy      1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVVQTDSIPNSPDNVPLKG 60
        |||||||
Db      1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVVQTDSIPNSPDNVPLKG 60
        |||||||

Qy      61 GCNSEDLLCILKRAPFKSWAYLOVAKHLNKTKLISWNKDGLHGVRYODGNLVIOFPGLY 120
        |||||||
Db      61 GCNSEDLLCILKRAPFKSWAYLOVAKHLNKTKLISWNKDGLHGVRYODGNLVIOFPGLY 120
        |||||||

Qy      121 FIICQLQFLVCPNNVDLKLELLINKHIKQAALVTTCESGMQTKHYVTONLSQFLLDYLQ 180
        |||||||
Db      121 FIICQLQFLVCPNNVDLKLELLINKHIKQAALVTTCESGMQTKHYVTONLSQFLLDYLQ 180
        |||||||

Qy      181 VNTTISVNDTFQYIDSTFTPLENVLSIFLYSNSD 215
        |||||||
Db      181 VNTTISVNDTFQYIDSTFTPLENVLSIFLYSNSD 215
        |||||||

RESULT      3
US-08-580-014-23
; Sequence 23, Application US/08580014
; Patent No. 5753203
; GENERAL INFORMATION:
;   APPLICANT: Goodwin, Raymond G.
;   APPLICANT: Smith, Craig A.
;   APPLICANT: Armitage, Richard J.
;   APPLICANT: Gruss, Hans-Jurgen
;   TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
;   NUMBER OF SEQUENCES: 23
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Kathryn A. Seese, Immunex Corporation
;     STREET: 51 University Street
;     CITY: Seattle
;     STATE: Washington
;     COUNTRY: USA
;     ZIP: 98101
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: Apple Macintosh
;     OPERATING SYSTEM: Apple 7.1
;     SOFTWARE: Microsoft Word, Version 5.1a
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/580,014
;     FILING DATE: 20-DEC-1995
;     CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/08/225,989
;     FILING DATE: 12 APRIL 1994
;     APPLICATION NUMBER: US 07/966,775
;     FILING DATE: 27-OCT-1992

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CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 215 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-580-014-23

Query Match 100.0%; Score 1118; DB 1; Length 215;  
Best Local Similarity 100.0%; Pred. No. 5.9e-114;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVPLKG 60  
Qy 61 GNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVRYQDGNLVIOFPGLY 120  
Db 61 GNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVRYQDGNLVIOFPGLY 120  
Qy 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKIKQALVTVCESGMOTKHVYQNLQSLFDLYLQ 180  
Db 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKIKQALVTVCESGMOTKHVYQNLQSLFDLYLQ 180  
Qy 181 VNTTISVNVDTFOYIDTSTFFPLENVLSIFLYNSD 215  
Db 181 VNTTISVNVDTFOYIDTSTFFPLENVLSIFLYNSD 215

RESULT 4  
US-09-079-785-23  
Sequence 23, Application US/09079785  
Patent No. 6143869  
GENERAL INFORMATION:  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
APPLICANT: Armitage, Richard J.  
APPLICANT: Gruss, Hans-Jurgen  
TITLE OF INVENTION: No. 6143869el Cytokine That Binds CD30  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1

SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,785  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,989  
FILING DATE: 12 APRIL 1994  
APPLICATION NUMBER: US 07/966,775  
FILING DATE: 27-OCT-1992  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 215 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-079-785-23

Query Match 100.0%; Score 1118; DB 4; Length 215;  
Best Local Similarity 100.0%; Pred. No. 5.9e-114;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVPLKG 60  
Db 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVPLKG 60  
Qy 61 GNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVRYQDGNLVIOFPGLY 120  
Db 61 GNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVRYQDGNLVIOFPGLY 120  
Qy 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKIKQALVTVCESGMOTKHVYQNLQSLFDLYLQ 180  
Db 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKIKQALVTVCESGMOTKHVYQNLQSLFDLYLQ 180  
Qy 181 VNTTISVNVDTFOYIDTSTFFPLENVLSIFLYNSD 215  
Db 181 VNTTISVNVDTFOYIDTSTFFPLENVLSIFLYNSD 215  
RESULT 5  
US-08-225-989-8  
Sequence 8, Application US/08225989  
Patent No. 5480981  
GENERAL INFORMATION:  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
APPLICANT: Armitage, Richard J.  
APPLICANT: Gruss, Hans-Jurgen  
TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:

RESULT 6  
US-08-570-923-8  
; Sequence 8, Application US/08570923  
; Patent No. 5677430

Qy	1	MHPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVPK	60
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Qy	61	GNCSDDLCLIKRAPFKSWAYLQVAKHLNKTLSNNKGILHGVRVQGNLVIQPPGL	120
Db	80	GNCSDDLCLIKRAPFKSWAYLQVAKHLNKTLSNNKGILHGVRVQGNLVIQPPGL	139
Qy	121	FIICQLFLVOCPPNNSVDLLELLINKHKIKQALVTVCSGSMQTKHYVQNLSOFLDYLQ	180
Db	140	FIICQLFLVOCPPNNSVDLLELLINKHKIKQALVTVCSGSMQTKHYVQNLSOFLDYLQ	199

QY 181 VNTTISVNDTFQYIDTSTFPLENVLISFLYSNSD 215  
Db 200 VNTTISVNDTFQYIDTSTFPLENVLISFLYSNSD 234  
RESULT 7  
US-08-580-014-8  
; Sequence 8, Application US/08580014  
; Patent No. 5753203  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/580,014  
; FILING DATE: 20-DEC-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 234 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-580-014-8

Query Match 100.0%; Score 1118; DB 1; Length 234;  
Best Local Similarity 100.0%; Pred. No. 6.6e-114;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHPVAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLPGK 60

Db 20 MHPVAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLPGK 79  
QY 61 GNCSEDLGILKRAPFKKSWAYLQVAKHLNKTLSNKNKGILHGVRYQDGNLVIQPPGLY 120  
Db 80 GNCSEDLGILKRAPFKKSWAYLQVAKHLNKTLSNKNKGILHGVRYQDGNLVIQPPGLY 139  
QY 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKKALVTVCSGMOVKHYQNLSQFLLDYLO 180  
Db 140 FIICQLQFLVQCPNNSVDLKLLELLINKHKKALVTVCSGMOVKHYQNLSQFLLDYLO 199  
QY 181 VNTTISVNDTFQYIDTSTFPLENVLISFLYSNSD 215  
Db 200 VNTTISVNDTFQYIDTSTFPLENVLISFLYSNSD 234  
RESULT 8  
US-09-079-785-8  
; Sequence 8, Application US/09079785  
; Patent No. 6143869  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 6143869el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/079,785  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 234 amino acids  
; TYPE: amino acid



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;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-079-785-8

Query Match 100.0%; Score 1118; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 6.6e-114; Indels 0; Gaps 0;
Matches 215; Conservative 0; Mismatches 0;

Qy 1 MHVPAGSVASHLGTTSRSFYLLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLKG 60
Dy 20 MHVPAGSVASHLGTTSRSFYLLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLKG 79

Qy 61 GNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSNKGILHGVRYQDGNLVIFQFGLY 120
Dy 80 GNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSNKGILHGVRYQDGNLVIFQFGLY 139

Qy 121 FTICQLQFLVQCPNNSVDLKLLELLINKHKQALVTVCSGDMOTKHVYQNLQSLDYLO 180
Dy 140 FTICQLQFLVQCPNNSVDLKLLELLINKHKQALVTVCSGDMOTKHVYQNLQSLDYLO 199

Qy 181 VNTTISVNVDTFQYIDTSTFPLENVLSIFLYNSD 215
Dy 200 VNTTISVNVDTFQYIDTSTFPLENVLSIFLYNSD 234

RESULT 9
US-08-225-989-19
; Sequence 19, Application US/08225989
; Patent No. 5480981
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-225-989-19

Query Match 72.9%; Score 814.5; DB 1; Length 220;
Best Local Similarity 70.6%; Pred. No. 6.5e-81;
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

Qy 1 MHVPAGSVAS-----HLGTTSSRSFYLLTATLALCLVFTVATIMVLVQRTDSIPNSPD 54
Dy 1 MOVQPGSVASPMRSPRMRSTSRSYFLSTTAL-VCLVVAVAILVLVYVOKKDSPTNTTE 59

Qy 55 NVPLKGGNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSNKGILHGVRYQDGNLV 114
Dy 60 KAPLKGNCSEDLICTLSTPSKKSWAYLQVSKHLNNTKLSNEDGTIHLIYQDGNLV 119

Qy 115 QPGLYFTICQLQFLVQCPNNSVDLKLLELLINKHKQALVTVCSGDMOTKHVYQNLQSL 174
Dy 120 QPGLYFTICQLQFLVQCPNNSVDLTLQLLINSKIKKOTLVTVCSGVQSKNIYQNLQSL 179

Qy 175 LLDYLVQVNTTISVNVDTFQYIDTSTFPLENVLSIFLYNSD 215
Dy 180 LLDYLVQVNTTISVNVDTFQYIDTSTFPLENVLSIFLYNSD 220

RESULT 10
US-08-570-923-19
; Sequence 19, Application US/08570923
; Patent No. 5677430
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,923
; FILING DATE: 12-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
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? ZIP: 95011
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? COMPUTER READABLE FORM:
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? MEDIUM TYPE: Floppy disk
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? COMPUTER: Apple Macintosh
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? OPERATING SYSTEM: Apple 7.1
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? SOFTWARE: Microsoft Word, Version 5.1a
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? CURRENT APPLICATION DATA:
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? APPLICATION NUMBER: US/08/580,014
?
? FILING DATE: 20-DEC-1995
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? CLASSIFICATION: 530
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? PRIOR APPLICATION DATA:
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? APPLICATION NUMBER: US/08/225,989
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RESULT 12  
 US-09-079-785-19  
 ; Sequence 19, Application US/09079785  
 ; Patent No. 6143869  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Goodwin, Raymond G.  
 ; APPLICANT: Smith, Craig A.  
 ; APPLICANT: Armitage, Richard J.  
 ; APPLICANT: Gruss, Hans-Jürgen  
 ; TITLE OF INVENTION: No. 6143869el Cytokine That Binds CD30  
 ; NUMBER OF SEQUENCES: 23  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
 ; STREET: 51 University Street  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; COUNTRY: USA  
 ; ZIP: 98101  
 ; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: Apple Macintosh  
;; OPERATING SYSTEM: Apple 7.1  
;; SOFTWARE: Microsoft Word, Version 5.1a  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/079,785  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/225,989  
;; FILING DATE: 12 APRIL 1994  
;; APPLICATION NUMBER: US 07/966,775  
;; FILING DATE: 27-OCT-1992  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 907,224  
;; FILING DATE: 01-JUL-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 899,660  
;; FILING DATE: 15-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 892,459  
;; FILING DATE: 02-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 889,717  
;; FILING DATE: 26-MAY-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Seese, Kathryn A.  
;; REGISTRATION NUMBER: 32,172  
;; REFERENCE/DOCKET NUMBER: 2804-E  
;; TELEPHONE: (206)587-0430  
;; TELEFAX: (206)233-0644  
;; TELEX: 756822  
;; INFORMATION FOR SEQ ID NO: 19:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 220 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-09-079-785-19

Query Match 72.9%; Score 814.5; DB 4; Length 220;  
Best Local Similarity 70.6%; Pred. No. 6.5e-81;  
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;  
QY 1 MHVPAGSVAS-----HLGTTSRSYFLTTATLALCLVFTVATIMVLVQRTDSIPNSPD 54  
DB 1 MQVQPGSVASPRWSTRPWRSTRSYFLSTAL-VCLVAVAILVLVQKDKSTPNTTE 59  
QY 55 NVPLKGGNCSEDLCLILKRAPFKKSWAYLQVAKHLNKTLSNKGDLHGVRQDGNLVI 114  
DB 60 KAPLKGNCSEDLFCTLKSTPSKSWAYLQVSKHLNKTLSNKGDLHGVRQDGNLVI 119  
QY 115 QPGLYFIICQLQFLVQCSPNNSVDLKLLELNKHIKQALVTVCESGMOTKHVYQNLISQF 174  
DB 120 QPGLYFIICQLQFLVQCSPNNSVDLKLLELNKHIKQALVTVCESGMOTKHVYQNLISQF 179  
QY 175 LLDYLVQNTTISVNDVTFQYIDTSTFPLENVLSIFLYSNSD 215  
DB 180 LLHYLVQNVSTISVRVDFQYIDVNTFPDLNVLVSFLYSSSD 220

RESULT 13  
US-08-225-989-6  
; Sequence 6, Application US/08225989  
; Patent No. 5480981  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen

;; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30  
;; NUMBER OF SEQUENCES: 23  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
;; STREET: 51 University Street  
;; CITY: Seattle  
;; STATE: Washington  
;; COUNTRY: USA  
;; ZIP: 98101  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: Apple Macintosh  
;; OPERATING SYSTEM: Apple 7.1  
;; SOFTWARE: Microsoft Word, Version 5.1a  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/225,989  
;; FILING DATE: 12 APRIL 1994  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/966,775  
;; FILING DATE: 27-OCT-1992  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 907,224  
;; FILING DATE: 01-JUL-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 899,660  
;; FILING DATE: 15-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 892,459  
;; FILING DATE: 02-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 889,717  
;; FILING DATE: 26-MAY-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Seese, Kathryn A.  
;; REGISTRATION NUMBER: 32,172  
;; REFERENCE/DOCKET NUMBER: 2804-E  
;; TELEPHONE: (206)587-0430  
;; TELEFAX: (206)233-0644  
;; TELEX: 756822  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 239 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-225-989-6

Query Match 72.9%; Score 814.5; DB 1; Length 239;  
Best Local Similarity 70.6%; Pred. No. 7.3e-81;  
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;  
QY 1 MHVPAGSVAS-----HLGTTSRSYFLTTATLALCLVFTVATIMVLVQRTDSIPNSPD 54  
DB 20 MQVQPGSVASPRWSTRPWRSTRSYFLSTAL-VCLVAVAILVLVQKDKSTPNTTE 78  
QY 55 NVPLKGGNCSEDLCLILKRAPFKKSWAYLQVAKHLNKTLSNKGDLHGVRQDGNLVI 114  
DB 79 KAPLKGNCSEDLFCTLKSTPSKSWAYLQVSKHLNKTLSNKGDLHGVRQDGNLVI 138  
QY 115 QPGLYFIICQLQFLVQCSPNNSVDLKLLELNKHIKQALVTVCESGMOTKHVYQNLISQF 174  
DB 139 QPGLYFIICQLQFLVQCSPNNSVDLKLLELNKHIKQALVTVCESGMOTKHVYQNLISQF 198  
QY 175 LLDYLVQNTTISVNDVTFQYIDTSTFPLENVLSIFLYSNSD 215  
DB 199 LLHYLVQNVSTISVRVDFQYIDVNTFPDLNVLVSFLYSSSD 239

RESULT 14



	Matches 156;	Conservative 26;	Mismatches 32;	Indels 7;	Gaps 2;
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Db	20	MQVQ	PCSVAS	PWRSTP	WSTSRSEYLTAL-VCLVAVAILLVVQKKDSTPNTTE 78
QY 55	NYPL	KGNC	SEDL	LCILK	RAPPKSWAYLQVAKHLNKTLSWNKDGILHGVRYQDGNLVI 114
Db	79	KAPL	KGNC	SEDL	FCTLKTSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIV 138
QY 115	QPGLY	FIIC	QFLV	QCENNS	VDLKLLELLINKHIKKQALVTVCESGMQTKHVIYQNLQSF 174
Db	139	QPGLY	FIIC	QFLV	QCENNSVDLTQLLLINSKIKKQTLVTVCESGVOSKNIYQNLQSF 198
QY 175	LDYLV	QVNT	TSVNV	DTFOY	IDTSTFPLENVLSIFLYSNSD 215
Db	199	LDYLV	QVNT	TSVNV	DTFOYIDTSTFPLENVLSIFLYSNSD 239

Search completed: September 5, 2001, 10:23:11  
 Job time: 86 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2001, 10:22:39 ; Search time 44.86 Seconds  
(without alignments)  
290.552 Million cell updates/sec

Title: US-09-628-126-23  
Perfect score: 1118  
Sequence: 1 MHVPAQSVASHLGTTSRVSF.....DTSTFPLENVLISFLYNSD 215

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1118	100.0	234	14 AAR45009	Sequence encoded b
3	814.5	72.9	220	14 AAR45006	Sequence encoded b
4	814.5	72.9	239	14 AAR45008	Sequence encoded b
5	741	66.3	143	21 AAB08276	Amino acid sequenc
6	608	54.4	143	21 AAB08277	Amino acid sequenc
7	115	10.3	279	17 AAR88357	Mouse Fas ligand.
8	112	10.0	179	16 AAR79069	Mouse Fas ligand.
9	112	10.0	279	16 AAR79098	Mouse Fas ligand.
10	108	9.7	143	21 AAB08266	Amino acid sequenc
11	106	9.5	138	16 AAR79068	Mouse Fas ligand (

12	104	9.3	137	16	AAR79067	Mouse Fas ligand (
13	102	9.1	279	16	AAR77282	Mouse Fas-L protei
14	97	8.7	268	19	AAW48953	Non-cleavable Fas
15	96.5	8.6	265	19	AAW48954	Non-cleavable Fas
16	95	8.5	180	18	AAW10875	FasL/lt-alpha hybr
17	93	8.3	216	19	AAW68412	Hybrid alpha-1-thy
18	92	8.2	378	18	AAW35864	Human FAS-ligand: I
19	91.5	8.2	261	20	AAV28597	Fas ligand (FasL)
20	91.5	8.2	281	21	AAW87581	Human Fas ligand (
21	91.5	8.2	376	21	AAV52588	Secreted modified
22	91	8.1	258	20	AAV04371	C-terminally delet
23	90.5	8.1	145	18	AAW35848	Human FAS-ligand d
24	90.5	8.1	151	18	AAW16687	Human Fas ligand (
25	90.5	8.1	178	16	AAR88308	Human FAS-ligand f
26	90.5	8.1	179	16	AAR79099	Human Fas ligand (
27	90.5	8.1	179	18	AAW11814	Human Fas ligand (
28	90.5	8.1	271	20	AAV28596	Fas ligand. Homo
29	90.5	8.1	277	20	AAV28595	Fas ligand (FasL)
30	90.5	8.1	277	20	AAV04372	Fas ligand (FasL)
31	90.5	8.1	281	16	AAR77281	Human Fas ligand d
32	90.5	8.1	281	16	AAR79097	Human Fas-L protei
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34	90.5	8.1	281	17	AAR88356	Human Fas ligand d
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36	90.5	8.1	281	19	AAW75959	Human Fas ligand.
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38	90.5	8.1	281	20	AAV28594	Wild type Fas liga
39	90.5	8.1	281	20	AAV04373	Human Fas ligand d
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#### ALIGNMENTS

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ID AAR45007 standard; Protein; 215 AA.  
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AC AAR45007;  
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DT 19-JUN-1994 (first entry)  
XX  
DE Sequence encoded by a human CD30-L cDNA clone.  
XX  
KW Hodgkin's disease; lymphoma; surface antigen; cytokine;  
KW CD30 ligand; CD30-L; TNF; NGF.  
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OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 22..43  
FT /label= transmembrane  
XX  
FT  
XX  
PN W09324135-A.  
XX  
PD 09-DEC-1993.  
XX  
PF 25-MAY-1993; 93WO-US04926.  
XX  
PR 26-MAY-1992; 92US-0889717.  
PR 02-JUN-1992; 92US-0892459.  
PR 15-JUN-1992; 92US-0899660.  
PR 01-JUL-1992; 92US-0907224.  
PR 27-OCT-1992; 92US-0966775.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Armitage RJ, Goodwin RG, Smith CA;

```

XX
DR WPI; 1993-405417/50.
DR N-PSDB; AAQ53536.
XX
XX New cytokine, CD30-L, which binds CD30 - used for developing
XX prods. for diagnosis, detection, purifications, research and
XX therapy
XX
XX Claim 15; Figure 5a; 59pp; English.
PS
PS CD30-L is a ligand for CD30, the 120kd surface antigen widely used
CC as a clinical marker for Hodgkin's lymphoma and related haematologic
CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
CC L and other derived prods. can be used for elucidating the roles
CC that CD30 and CD30-L may play in the immune system and for diagnosis
CC and therapy. It can be isolated as follows. A cDNA library prepd. from
CC the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion
CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L.
CC This cDNA can then be used as a probe to screen a human PBL cDNA
CC library to obtain cDNA encoding human CD30-L.
XX
XX Sequence 215 AA;
XX
Query Match 100.0%; Score 1118; DB 14; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.7e-116;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHVPAGSVASHLGTTSRSYFLTTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLKLG 60
Db 1 mhvpagsvashlgttsrsyflttatlalclvftvatimvlvqrtdsipnsdpnvpk 60
QY 61 GNCSEDLICILKRAPFKSWAYLQVAKHLNKTLSWNKDGILHGVRYQDGNLVIQFPGLY 120
Db 61 gncsedlilcilkrapfkswaylqvakhlnktlswnkdgilhgvryqdglnviqfp 120
QY 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKKQALVTVCESGMOTKHVYQNLSQFLLDYLQ 180
Db 121 fiicqlqlvqcpnnsvdllkllinkhikkqalvtvcsgmqt khvyqnlsgflldylq 180
QY 181 VNTTISVNVDTFQYIDTSTFPLENVLISFLYSNSD 215
Db 181 vnttisvndvtfqyidstfplenvlsiflynsd 215
RESULT 2
AAR45009
ID AAR45009 standard; Protein; 234 AA.
XX
XX AAR45009;
XX
XX 19-JUN-1994 (first entry)
XX
XX Sequence encoded by a human CD30-L cDNA clone
DE encoding additional N-terminal amino acids.
XX
XX Hodgkin's disease; lymphoma; surface antigen; cytokine;
KW CD30 ligand; CD30-L; TNF; NGF.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH 41..62
FT /label= Transmembrane
XX
XX WO9324135-A.
XX
XX 09-DEC-1993.
XX
XX 25-MAY-1993; 93WO-US04926.
XX
XX 26-MAY-1992; 92US-0889717.
PR 02-JUN-1992; 92US-0892459.

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PR 15-JUN-1992; 92US-0899660.
PR 01-JUL-1992; 92US-0907224.
PR 27-OCT-1992; 92US-0966775.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Armitage RJ, Goodwin RG, Smith CA;
PI WPI; 1993-405417/50.
DR N-PSDB; AAQ53538.
XX
XX New cytokine, CD30-L, which binds CD30 - used for developing
XX prods. for diagnosis, detection, purifications, research and
XX therapy
XX
XX Claim 15; Figure 7a; 59pp; English.
PS
PS CD30-L is a ligand for CD30, the 120kd surface antigen widely used
CC as a clinical marker for Hodgkin's lymphoma and related haematologic
CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
CC L and other derived prods. can be used for elucidating the roles
CC that CD30 and CD30-L may play in the immune system and for diagnosis
CC and therapy. It can be isolated as follows. A cDNA library prepd. from
CC the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion
CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L
CC (AAQ53535). This cDNA can then be used as a probe to screen a human PBL
CC cDNA library to obtain cDNA encoding human CD30-L (AAQ53536). An
CC anchored PCR technique was employed to isolate CD30-L human and murine
CC clones containing an additional 19 N-terminal amino acid sequence
CC (AAQ53537, AAQ53538).
XX
XX Sequence 234 AA;
XX
Query Match 100.0%; Score 1118; DB 14; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.9e-116;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHVPAGSVASHLGTTSRSYFLTTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLKLG 60
Db 20 mhvpagsvashlgttsrsyflttatlalclvftvatimvlvqrtdsipnsdpnvpk 79
QY 61 GNCSEDLICILKRAPFKSWAYLQVAKHLNKTLSWNKDGILHGVRYQDGNLVIQFPGLY 120
Db 80 gncsedlilcilkrapfkswaylqvakhlnktlswnkdgilhgvryqdglnviqfp 139
QY 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKKQALVTVCESGMOTKHVYQNLSQFLLDYLQ 180
Db 140 fiicqlqlvqcpnnsvdllkllinkhikkqalvtvcsgmqt khvyqnlsgflldylq 199
QY 181 VNTTISVNVDTFQYIDTSTFPLENVLISFLYSNSD 215
Db 200 vnttisvndvtfqyidstfplenvlsiflynsd 234
RESULT 3
AAR45006
ID AAR45006 standard; Protein; 220 AA.
XX
XX AAR45006;
XX
XX 19-JUN-1994 (first entry)
XX
XX Sequence encoded by a murine CD30-L cDNA clone.
DE
XX Hodgkin's disease; lymphoma; surface antigen; cytokine;
KW CD30 ligand; CD30-L; TNF; NGF.
XX
XX Acomys cahirinus.
XX
XX Key Location/Qualifiers
FH 28..48
FT /label= transmembrane

```

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XX WO9324135-A.
XX
XX PD 09-DEC-1993.
XX
XX PF 25-MAY-1993; 93WO-US04926.
XX
XX PR 26-MAY-1992; 92US-0889717.
XX
XX PR 02-JUN-1992; 92US-0892459.
XX
XX PR 15-JUN-1992; 92US-0899660.
XX
XX PR 01-JUL-1992; 92US-0907224.
XX
XX PR 27-OCT-1992; 92US-0966775.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Armitage RJ, Goodwin RG, Smith CA;
XX
XX WPI; 1993-405417/50.
XX
XX DR N-PSDB; AAQ53535.
XX
XX New cytokine, CD30-L, which binds CD30 - used for developing
XX prods. for diagnosis, detection, purifications, research and
XX therapy
XX
XX Claim 15; Figure 3a; 59pp; English.
XX
XX CD30-L is a ligand for CD30, the 120kd surface antigen widely used
XX as a clinical marker for Hodgkin's lymphoma and related haematologic
XX malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
XX L and other derived prods. can be used for elucidating the roles
XX that CD30 and CD30-L may play in the immune system and for diagnosis
XX and therapy. It can be isolated as follows. A cDNA library prepd. from
XX the murine helper T-cell line 7B9 is screened with a CD30/FC fusion
XX protein labelled with (125)I to obtain cDNA encoding murine CD30-L.
XX This cDNA can then be used as a probe to screen a human PBL cDNA
XX library to obtain cDNA encoding human CD30-L.
XX
XX Sequence 220 AA;
XX
XX Query Match 72.9%; Score 814.5; DB 14; Length 220;
XX Best Local Similarity 70.6%; Pred. No. 1.2e-82;
XX Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;
XX
XX QY 1 MHVPAGSVAS-----HLGTTSRSYFYLTATLALCLVFTVATIMVLVQRTDSIPNSPD 54
XX | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
XX 1 mqvpgsvasprwstrprwstrsrsfyfisttal-vcilvvavailvlvqkdstpntte 59
XX
XX QY 55 NVPLKGGNCSEDLCLILKRAPKKSWAYLQVAKHLNKTLSWNKDGILHGVRQDGNLVI 114
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 60 kaplkgncsedlftclktstpskkswaylqvskhlnntklswnedgtihglyqdnliv 119
XX
XX QY 115 QPGLYFIICOLQFLVQCPCNNNSVDLKLLELLINKHKIKQALVTVCESGMOTKHVYQNLISQF 174
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 120 qfpglyfivcqlqflvqcshsvdltclqllnskikkktlvtvcesgvqskniyqnsqf 179
XX
XX QY 175 LLDYLVQVNTTISVNVDTFYIDTSTFPLENVLISFLYSNSD 215
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 180 llhylvqvnstisvrndfnfyvdtntfpldnvlsvflysssd 220
XX
XX RESULT 4
XX AAR45008
XX ID AAR45008 standard; Protein; 239 AA.
XX
XX AC AAR45008;
XX
XX DT 19-JUN-1994 (first entry)
XX
XX DE Sequence encoded by a murine CD30-L cDNA clone
XX encoding additional N-terminal amino acids.
XX
XX KW Hodgkin's disease; lymphoma; surface antigen; cytokine;

```

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KW CD30 ligand; CD30-L; TNF; NGF.
XX
XX OS Acomys cahirinus.
XX
XX FH Key Location/Qualifiers
XX Region 47..67
XX FT /label= Transmembrane
XX
XX PN WO9324135-A.
XX
XX PD 09-DEC-1993.
XX
XX PF 25-MAY-1993; 93WO-US04926.
XX
XX PR 26-MAY-1992; 92US-0889717.
XX
XX PR 02-JUN-1992; 92US-0892459.
XX
XX PR 15-JUN-1992; 92US-0899660.
XX
XX PR 01-JUL-1992; 92US-0907224.
XX
XX PR 27-OCT-1992; 92US-0966775.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Armitage RJ, Goodwin RG, Smith CA;
XX
XX WPI; 1993-405417/50.
XX
XX DR N-PSDB; AAQ53537.
XX
XX New cytokine, CD30-L, which binds CD30 - used for developing
XX prods. for diagnosis, detection, purifications, research and
XX therapy
XX
XX Claim 15; Figure 6a; 59pp; English.
XX
XX CD30-L is a ligand for CD30, the 120kd surface antigen widely used
XX as a clinical marker for Hodgkin's lymphoma and related haematologic
XX malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
XX L and other derived prods. can be used for elucidating the roles
XX that CD30 and CD30-L may play in the immune system and for diagnosis
XX and therapy. It can be isolated as follows. A cDNA library prepd. from
XX the murine helper T-cell line 7B9 is screened with a CD30/FC fusion
XX protein labelled with (125)I to obtain cDNA encoding murine CD30-L
XX (AAQ53535). This cDNA can then be used as a probe to screen a human PBL
XX cDNA library to obtain cDNA encoding human CD30-L (AAQ53536). An
XX anchored PCR technique was employed to isolate CD30-L human and murine
XX clones containing an additional 19 N-terminal amino acid sequence
XX (AAQ53537, AAQ53538).
XX
XX Sequence 239 AA;
XX
XX Query Match 72.9%; Score 814.5; DB 14; Length 239;
XX Best Local Similarity 70.6%; Pred. No. 1.3e-82;
XX Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;
XX
XX QY 1 MHVPAGSVAS-----HLGTTSRSYFYLTATLALCLVFTVATIMVLVQRTDSIPNSPD 54
XX | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
XX 20 mqvpgsvasprwstrprwstrsrsfyfisttal-vcilvvavailvlvqkdstpntte 78
XX
XX QY 55 NVPLKGGNCSEDLCLILKRAPKKSWAYLQVAKHLNKTLSWNKDGILHGVRQDGNLVI 114
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 79 kaplkgncsedlftclktstpskkswaylqvskhlnntklswnedgtihglyqdnliv 138
XX
XX QY 115 QPGLYFIICOLQFLVQCPCNNNSVDLKLLELLINKHKIKQALVTVCESGMOTKHVYQNLISQF 174
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 139 qfpglyfivcqlqflvqcshsvdltclqllnskikkktlvtvcesgvqskniyqnsqf 198
XX
XX QY 175 LLDYLVQVNTTISVNVDTFYIDTSTFPLENVLISFLYSNSD 215
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 199 llhylvqvnstisvrndfnfyvdtntfpldnvlsvflysssd 239
XX
XX RESULT 5
XX AAB08276

```



ID AAB08276 standard; Protein; 143 AA.  
 AC AAB08276;  
 XX  
 XX  
 DT  
 XX  
 XX  
 DE 04-DEC-2000 (first entry)  
 XX  
 XX Amino acid sequence of a human TNF ligand CD30L.  
 DE AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;  
 KW type II transmembrane protein; B cell stimulatory factor;  
 KW inflammatory disorder; immune disorder; rheumatoid arthritis;  
 KW lupus and graft versus host disease.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200047740-A2.  
 XX  
 XX 17-AUG-2000.  
 PD  
 XX  
 XX 11-FEB-2000; 2000WO-US03653.  
 XX  
 XX 12-FEB-1999; 99US-0119906.  
 XX  
 XX 18-NOV-1999; 99US-0166271.  
 PR  
 XX (AMGE-) AMGEN INC.  
 PA  
 XX Boyle WJ, Hsu H;  
 XX  
 XX WPI; 2000-558217/51.  
 DR  
 XX Novel polypeptides comprising tumour necrosis factor ligand family  
 PT proteins, useful for treating inflammatory and immune disorders, e.g.  
 PT rheumatoid arthritis -  
 PT  
 XX  
 XX Claim 14; Fig 9; 71pp; English.  
 PS  
 XX AAB08265-83 represent tumour necrosis factor (TNF) ligands. The  
 CC specification describes an AGP-3 polypeptide, which is TNF ligand  
 CC family member. AGP-3 is a type II transmembrane protein, and is a  
 CC potent B cell stimulatory factor. Expression of AGP-3 correlates to  
 CC increases in the number of B cells and immunoglobulins produced.  
 CC AGP-3 proteins, antibodies, and nucleic acids may be used to treat  
 CC inflammatory and immune disorders, e.g. rheumatoid arthritis,  
 CC Crohn's disease, lupus and graft versus host disease. The nucleic  
 CC acids may be used to regulate the expression of an AGP-3 related  
 CC protein. The AGP-3 proteins, antibodies and nucleic acids are also  
 CC useful for the detection of AGP-3 agonists, antagonists and  
 CC characterizing interactions with AGP-3 related proteins.  
 XX  
 XX Sequence 143 AA;  
 SQ  
 Query Match 66.3%; Score 741; DB 21; Length 143;  
 Best Local Similarity 99.3%; Pred. No. 1e-74;  
 Matches 142; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 73 RAPEKSWAYLQVAKHLNKTLSWKNKDGILHGVRYODGNLVTFQPGLYFIICOLQFLVOC 132  
 Db 1 rapfkswaylqvakhlnktlswnkdgilhgvryqdglnlvtfpglyfiicqlqlfvqc 60  
 QY 133 PNNVDLKLLELLINKHKIKKQALVTVCESGMQTKHYQNLISQFLLDYLOVNTTISVNDTF 192  
 Db 61 pnnsvdlkllinkhikkqalvtvcsgmqtkhyqnlisqfildylqvmttisvndtf 120  
 QY 193 QYIDTSTFPLENLVSIFLYNSND 215  
 Db 121 qyidstfplenvlsiflynsnd 143  
 RESULT 6  
 AAB08277  
 ID AAB08277 standard; Protein; 143 AA.  
 XX

AC AAB08277;  
 XX  
 XX 04-DEC-2000 (first entry)  
 XX  
 XX Amino acid sequence of a mouse TNF ligand CD30L.  
 XX  
 XX AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;  
 KW type II transmembrane protein; B cell stimulatory factor;  
 KW inflammatory disorder; immune disorder; rheumatoid arthritis;  
 KW lupus and graft versus host disease.  
 XX  
 XX Mus sp.  
 OS  
 XX  
 XX WO200047740-A2.  
 XX  
 XX 17-AUG-2000.  
 PD  
 XX  
 XX 11-FEB-2000; 2000WO-US03653.  
 XX  
 XX 12-FEB-1999; 99US-0119906.  
 XX  
 XX 18-NOV-1999; 99US-0166271.  
 PR  
 XX (AMGE-) AMGEN INC.  
 PA  
 XX  
 XX Boyle WJ, Hsu H;  
 XX  
 XX WPI; 2000-558217/51.  
 DR  
 XX Novel polypeptides comprising tumour necrosis factor ligand family  
 PT proteins, useful for treating inflammatory and immune disorders, e.g.  
 PT rheumatoid arthritis -  
 PT  
 XX  
 XX Claim 14; Fig 9; 71pp; English.  
 PS  
 XX AAB08265-83 represent tumour necrosis factor (TNF) ligands. The  
 CC specification describes an AGP-3 polypeptide, which is TNF ligand  
 CC family member. AGP-3 is a type II transmembrane protein, and is a  
 CC potent B cell stimulatory factor. Expression of AGP-3 correlates to  
 CC increases in the number of B cells and immunoglobulins produced.  
 CC AGP-3 proteins, antibodies, and nucleic acids may be used to treat  
 CC inflammatory and immune disorders, e.g. rheumatoid arthritis,  
 CC Crohn's disease, lupus and graft versus host disease. The nucleic  
 CC acids may be used to regulate the expression of an AGP-3 related  
 CC protein. The AGP-3 proteins, antibodies and nucleic acids are also  
 CC useful for the detection of AGP-3 agonists, antagonists and  
 CC characterizing interactions with AGP-3 related proteins.  
 XX  
 XX Sequence 143 AA;  
 SQ  
 Query Match 54.4%; Score 608; DB 21; Length 143;  
 Best Local Similarity 78.0%; Pred. No. 6.6e-60;  
 Matches 110; Conservative 19; Mismatches 12; Indels 0; Gaps 0;  
 QY 75 PFKKSWAYLQVAKHLNKTLSWKNKDGILHGVRYODGNLVTFQPGLYFIICOLQFLVOC 134  
 Db 3 pskkswaylqvakhlnktlswnkdgilhgvryqdglnlvtfpglyfiicqlqlfvqcsn 62  
 QY 135 NSVDLKLLELLINKHKIKKQALVTVCESGMQTKHYQNLISQFLLDYLOVNTTISVNDTF 194  
 Db 63 hysvdltlqlilnsikkqtlvtvcsgvqsknlisqfildylqvnstisvrvdnfq 122  
 QY 195 IDTSTFPLENLVSIFLYNSND 215  
 Db 123 vdtntfpldnvlsfilyssnd 143  
 RESULT 7  
 AAB88357  
 ID AAB88357 standard; Protein; 279 AA.  
 XX  
 XX AAR88357;  
 XX

DT 15-OCT-1995 (first entry)  
 XX Mouse.Fas ligand.  
 DE  
 XX Fas ligand; transplant rejection; autoimmune disease; diabetes;  
 KW inflammation; graft rejection; rheumatoid arthritis; allergy;  
 KW cystic fibrosis; multiple sclerosis.  
 XX  
 XX Mus musculus.  
 OS  
 XX Key Location/Qualifiers  
 FH Peptide 101..279  
 FT /label= soluble mouse Fas ligand  
 FT  
 XX WO9532627-A1.  
 PN  
 XX  
 XX 07-DEC-1995.  
 PD  
 XX  
 XX 26-MAY-1995; 95WO-US06742.  
 PF  
 XX 26-JAN-1995; 95US-0378507.  
 PR  
 XX 27-MAY-1994; 94US-0250478.  
 PR  
 XX (COLS ) UNIV COLORADO.  
 PA  
 XX Bellgrau D, Duke RC;  
 PI WPI; 1996-030252/03.  
 XX N-PSDB; AAT09678.  
 DR  
 XX Use of Fas ligand - for suppressing lymphocyte-mediated immune  
 PT responses, e.g. transplant rejection or auto-immune conditions  
 PT  
 XX Claim 6; Fig.1; 5ipp; English.  
 PS  
 XX The expressed protein can be used to suppress and prevent  
 CC T-lymphocyte-mediated transplant or graft rejection, T-lymphocyte-  
 CC mediated disease recurrence or to treat T-lymphocyte-mediated  
 CC diseases. It can be used to treat diabetes, rheumatoid arthritis,  
 CC multiple sclerosis, cystic fibrosis or allergies.  
 CC  
 XX Sequence 279 AA;  
 SQ  
 Query Match 10.3%; Score 115; DB 17; Length 279;  
 Best Local Similarity 23.2%; Pred. NO. 0.00015;  
 Matches 39; Conservative 29; Mismatches 58; Indels 42; Gaps 6;  
 QY 33 FTVATIMVLVQRTSDIPNSPDNVPKGGNCSEDLICILKRAPFKKSWAYLQVAKHLNKT 92  
 Db 115 ftnqskvssfekqianpstpe-----kkep--rsvahltgnphrsi 156  
 Db  
 QY 93 KLSWKNK---DGLHGVRYQDGNLVIQFPGLYFIICQLQFLVQ-CPNNSVDLKLELLINKH 148  
 Db 157 plewedtygtalisgvkykkggvinetglyfyvskvyfrgscnqplnhkvymrnsky 216  
 QY 149 -----IKKQALVTVCESGM-----QTKHVVYQNLSQL 176  
 Db 217 pedlvimeqkrlnycttggiwahssylgavfnltsadhlvynisqlsl 264  
 RESULT 8  
 AAR79069  
 ID AAR79069 standard; Protein; 179 AA.  
 XX  
 XX AAR79069;  
 XX  
 XX 22-FEB-1996 (first entry)  
 DT  
 XX Mouse Fas ligand (partial sequence).  
 DE  
 XX Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;  
 KW Fas cell surface antigen; Fas-L; mouse.  
 KW

XX Mus musculus.  
 OS  
 XX WO9513293-A1.  
 PN  
 XX 18-MAY-1995.  
 PD  
 XX 10-NOV-1994; 94WO-JP01899.  
 PF  
 XX 18-OCT-1994; 94JP-0278378.  
 PR 10-NOV-1993; 93JP-0305975.  
 PR 13-DEC-1993; 93JP-0342526.  
 PR 18-MAR-1994; 94JP-0074344.  
 PR 08-JUL-1994; 94JP-0180955.  
 PR 07-SEP-1994; 94JP-0239363.  
 XX  
 XX (MOCH ) MOCHIDA PHARM CO LTD.  
 PA (OSAB-) OSAKA BIOSCIENCE INST.  
 PA  
 XX Nagata S, Nakamura N, Suda T, Takahashi T;  
 PI WPI; 1995-194031/25.  
 XX N-PSDB; AAQ99498.  
 DR  
 XX Peptide which binds to Fas antigen, and antibody reactive with it  
 PT for treatment and diagnosis of viral or auto-immune diseases  
 PT  
 XX Claim 11; Page 222-224; 300pp; Japanese.  
 PS  
 XX Fas ligands or active fragments able to induce apoptosis in cells  
 CC which express the Fas cell surface antigen are claimed. The  
 CC proteins are isolated from human, rat and mouse sources. The present  
 CC sequence represents part of the mouse Fas ligand.  
 CC  
 XX Sequence 179 AA;  
 SQ  
 Query Match 10.0%; Score 112; DB 16; Length 179;  
 Best Local Similarity 22.6%; Pred. NO. 0.00018;  
 Matches 38; Conservative 30; Mismatches 58; Indels 42; Gaps 6;  
 QY 33 FTVATIMVLVQRTSDIPNSPDNVPKGGNCSEDLICILKRAPFKKSWAYLQVAKHLNKT 92  
 Db 15 ftnqskvssfekqianpstpe-----kkep--rsvahltgnphrsi 56  
 Db  
 QY 93 KLSWKNK---DGLHGVRYQDGNLVIQFPGLYFIICQLQFLVQ-CPNNSVDLKLELLINKH 148  
 Db 57 plewedtygtalisgvkykkggvinetglyfyvskvyfrgscnqplnhkvymrnsky 116  
 QY 149 -----IKKQALVTVCESGM-----QTKHVVYQNLSQL 176  
 Db 117 pedlvimeqkrlnycttggiwahssylgavfnltsadhlvynisqlsl 164  
 RESULT 9  
 AAR79098  
 ID AAR79098 standard; Protein; 279 AA.  
 XX  
 XX AAR79098;  
 XX  
 XX 21-FEB-1996 (first entry)  
 DT  
 XX Mouse Fas ligand.  
 DE  
 XX Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;  
 KW Fas cell surface antigen; Fas-L; mouse.  
 KW  
 XX Mus musculus.  
 OS  
 XX Key Location/Qualifiers  
 FH Key 25..78  
 FT Region /label= proline-rich  
 FT Domain 79..100



DE Mouse Fas ligand (partial sequence).  
 XX Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;  
 KW Fas cell surface antigen; Fas-L; mouse.  
 XX Mus musculus.  
 OS  
 XX  
 XX  
 PN WO9513293-A1.  
 XX  
 XX 18-MAY-1995.  
 PD  
 XX  
 XX 10-NOV-1994; 94WO-JP01899.  
 XX  
 XX 18-OCT-1994; 94JP-0278378.  
 PR 10-NOV-1993; 93JP-0305975.  
 PR 13-DEC-1993; 93JP-0342526.  
 PR 18-MAR-1994; 94JP-0074344.  
 PR 08-JUL-1994; 94JP-0180955.  
 PR 07-SEP-1994; 94JP-0239363.  
 XX  
 XX (MOCH) MOCHIDA PHARM CO LTD.  
 PA (OSAB-) OSAKA BIOSCIENCE INST.  
 XX  
 XX Nagata S, Nakamura N, Suda T, Takahashi T;  
 PI  
 XX WPI; 1995-194031/25.  
 DR N-PSDB; AAQ99497.  
 XX  
 XX Peptide which binds to Fas antigen, and antibody reactive with it -  
 PT for treatment and diagnosis of viral or auto:immune diseases  
 PT  
 XX Claim 10; Page 221-222; 300pp; Japanese.  
 PS  
 XX Fas ligands or active fragments able to induce apoptosis in cells  
 CC which express the Fas cell surface antigen are claimed. The  
 CC proteins are isolated from human, rat and mouse sources. The present  
 CC sequence represents part of the mouse Fas ligand.  
 XX  
 XX Sequence 138 AA;  
 SQ  
 Query Match 9.5%; Score 106; DB 16; Length 138;  
 Best Local Similarity 25.2%; Pred. NO. 0.00056;  
 Matches 31; Conservative 22; Mismatches 46; Indels 24; Gaps 4;  
 QY 78 KSWAYLQVAKHLNKTLSWKNK---DGLHGVRVYQDGNLVIOFPGLYFIICQLQFLVQ-CP 133  
 Db 1 rsvahltgnphsrsipledtygtalisgvykkgglvlnetglyfyvskvyfrgscn 60  
 QY 134 NNSVDLKLELLINKH-----IKKQALVTVCESGM-----QTKHVTYONLSQ 173  
 Db 61 ngplnhkvymrnskyppedivlmeekrlnycttgqiwahssylgavfnltsadhllyvnisq 120  
 QY 174 FLL 176  
 Db 121 ls1 123  
 RESULT 12  
 AAR79067  
 ID AAR79067 standard; Protein; 137 AA.  
 XX  
 AC AAR79067;  
 XX  
 DT 22-FEB-1996 (first entry)  
 XX  
 DE Mouse Fas ligand (partial sequence).  
 XX  
 KW Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;  
 KW Fas cell surface antigen; Fas-L; mouse.  
 XX  
 OS Mus musculus.

PN WO9513293-A1.  
 XX  
 PD 18-MAY-1995.  
 XX  
 XX 10-NOV-1994; 94WO-JP01899.  
 XX  
 XX 18-OCT-1994; 94JP-0278378.  
 PR 10-NOV-1993; 93JP-0305975.  
 PR 13-DEC-1993; 93JP-0342526.  
 PR 18-MAR-1994; 94JP-0074344.  
 PR 08-JUL-1994; 94JP-0180955.  
 PR 07-SEP-1994; 94JP-0239363.  
 XX  
 XX (MOCH) MOCHIDA PHARM CO LTD.  
 PA (OSAB-) OSAKA BIOSCIENCE INST.  
 XX  
 XX Nagata S, Nakamura N, Suda T, Takahashi T;  
 PI  
 XX WPI; 1995-194031/25.  
 DR N-PSDB; AAQ99496.  
 XX  
 XX Peptide which binds to Fas antigen, and antibody reactive with it -  
 PT for treatment and diagnosis of viral or auto:immune diseases  
 PT  
 XX Claim 9; Page 219-221; 300pp; Japanese.  
 PS  
 XX Fas ligands or active fragments able to induce apoptosis in cells  
 CC which express the Fas cell surface antigen are claimed. The  
 CC proteins are isolated from human, rat and mouse sources. The present  
 CC sequence represents part of the mouse Fas ligand.  
 XX  
 XX Sequence 137 AA;  
 SQ  
 Query Match 9.3%; Score 104; DB 16; Length 137;  
 Best Local Similarity 25.4%; Pred. NO. 0.00093;  
 Matches 31; Conservative 21; Mismatches 46; Indels 24; Gaps 4;  
 QY 79 SWAYLQVAKHLNKTLSWKNK---DGLHGVRVYQDGNLVIOFPGLYFIICQLQFLVQ-CPN 134  
 Db 1 svahltgnphsrsipledtygtalisgvykkgglvlnetglyfyvskvyfrgscn 60  
 QY 135 NSVDLKLELLINKH-----IKKQALVTVCESGM-----QTKHVTYONLSQF 174  
 Db 61 qplnhkvymrnskyppedivlmeekrlnycttgqiwahssylgavfnltsadhllyvnisq 120  
 QY 175 LL 176  
 Db 121 sl 122  
 RESULT 13  
 AAR77282  
 ID AAR77282 standard; Protein; 279 AA.  
 XX  
 AC AAR77282;  
 XX  
 DT 05-DEC-1995 (first entry)  
 XX  
 DE Mouse Fas-L protein.  
 XX  
 KW Fas ligand; Fas-L; cell surface protein; autoimmune disease;  
 KW self-tolerance.  
 XX  
 OS Mus sp.  
 XX  
 XX Key Location/Qualifiers  
 FH 1..78  
 FT Domain /label= Cytoplasmic\_domain  
 FT 79..103 /label= Transmembrane\_domain  
 FT 104..279 /label= Extracellular\_domain  
 FT

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PN      WO9821232-A2.
XX
PD      22-MAY-1998.
XX
XX      13-NOV-1997;   97WO-US20864.
PF
XX      12-NOV-1997;   97US-0968686.
PR      13-NOV-1996;    96US-0030871.
PR      10-FEB-1997;   97US-0039972.
XX
XX      (CHIR ) CHIRON CORP.
PA
XX      Chu K;
PI
XX      WPI; 1998-297861/26.
DR      N-PSDB; AAV32622.
XX
XX      New DNA encoding Fas ligand agonist including, e.g. deletion -
PT      useful for, e.g. treating auto-immune diseases or transplant
PT      rejection
PT
XX      Claim 4; Pages 62-63; 72pp; English.
PS
XX
CC      The present sequence represents a non-cleavable Fas ligand 1306142
CC      deletion mutein. Fas ligand deletion mutein can be expressed in
CC      cells transfected with the DNA (AAV32622) coding for the mutant protein.
CC      These cells, expressing the mutant Fas ligand in a non-cleavable form,
CC      are claimed to be useful in vitro to identify cells that express Fas
CC      and, in vivo or in vitro, for reducing proliferation of Fas-expressing
CC      cells. The DNA encoding the Fas ligand mutant is claimed to be
CC      useful in gene therapy procedures and for the treatment of autoimmune
CC      diseases, e.g. multiple sclerosis, erythematosis, rheumatoid arthritis,
CC      glomerulonephritis, myasthenia gravis and transplant rejection.
XX
XX      Sequence 268 AA;
SQ
Query Match          8.7%; Score 97; DB 19; Length 268;
Best Local Similarity 22.4%; Pred. No. 0.015;
Matches 45; Conservative 27; Mismatches 55; Indels 74; Gaps 9;

Qy      49 IPNSPDNVPL-----KGGNCSEDLCLL-----KRA 74
Db      54 lpppeppppplpplpplkgrnhstg-lclvmffmvalvglgimqflhlqkela 112
Qy      75 PFKKSWAYLQVAKHLNKTG-----LSWKD-GI--LHGVRVODGNLVIOF 116
Db      113 elrëstqmtasslekrlrvahlgtksrsrsmplewedyglvlsgvykkggvline 172
Qy      117 PGLYFIICQLFLVQ-CPNNSVDLKLELLLNKH-----IKQALVTVCESGM----- 162
Db      173 tglyfyyskyfrygscnnlplshkvymrnskypqdilvmmegkmmsycttgqmwarssyl 232
Qy      163 -----OTKHVVYNLSQFLL 176
Db      233 gavnlttsadhlyvnvselsl 253

RESULT 15
AAW48954
ID      AAW48954 standard; Protein; 265 AA.
XX
XX      AAW48954;
AC
XX
DT      23-SEP-1998 (first entry)
XX
XX      Non-cleavable Fas ligand 1306145 deletion mutein.
XX
KW      Non-cleavable Fas ligand 1306145 deletion mutein; Fas; erythematosis;
KW      gene therapy; autoimmune disease; multiple sclerosis;
KW      rheumatoid arthritis; myasthenia gravis; transplant rejection;
KW      glomerulonephritis.
XX

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Search completed: September 5, 2001, 10:22:40  
Job time: 55 sec